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OM nucleic - nucleic search, using sw model

Run on: September 11, 2005, 22:05:26 ; Search time 1426.99 Seconds  
(without alignments)  
15416.180 Million cell updates/sec

Title:	US-10-758-799-2
Perfect score:	454
Sequence:	1 GTAACACACCCGCCCTTC.....CGTGGAGCTTTTGTAG 454

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

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Searched:      4708233  segs, 24227607955  residues
Total number of hits satisfying chosen parameters:  9416466
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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13: gb_un: *
14: gb_vi: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	454	100.0	454	6	A94724	A94724 Sequence 2
2	454	100.0	454	6	AR559744	AR559744 Sequence
3	454	100.0	454	6	BD128390	BD128390 Corin H3C
4	454	100.0	1565	6	A94725	A94725 Sequence 5
5	454	100.0	1565	6	AR559745	AR559745 Sequence
6	454	100.0	1565	6	BD128391	BD128391 Corin H3C
7	403.4	88.9	4895	12	A1452735	A1452735 Reporte
8	382.2	84.2	470	6	AX555557	AX555557 Sequence
9	379.4	83.6	623	6	AX467609	AX467609 Sequence
10	379.4	83.6	623	8	OSACRT1	K63830 O. salivaria A150114 Sequence 5
11	379.4	83.6	1392	6	IS0115	IS0115 Sequence 7
12	379.4	83.6	1404	6	IS0115	IS0115 Sequence 7
13	379.4	83.6	2199	6	IS0113	IS0113 Sequence 4
14	379.4	83.6	5643	6	IS0112	IS0112 Sequence 5
15	357.4	78.7	9359	6	AX384394	AX384394 Sequence
16	357.4	78.7	9359	6	AX473364	AX473364 Sequence
17	355.8	78.4	3039	6	AR271021	AR271021 Sequence
18	355.8	78.4	3039	6	AR271022	AR271022 Sequence
19	355.8	78.4	3044	6	AR271033	AR271033 Sequence

20	355.8	78.4	345.0	6	AR271020	Sequence
21	355.8	78.4	345.5	6	AR271032	Sequence
22	355.8	78.4	345.9	6	AR271023	Sequence
23	348	76.7	403.2	6	A71435	Sequence 5
24	348	76.7	403.2	6	AR207453	Sequence
25	348	76.7	403.2	6	AR564463	Sequence
26	348	76.7	403.2	6	BD069509	Improved
27	348	76.7	685.5	6	AX093008	Sequence
28	348	76.7	754.5	6	AX840288	Sequence
29	348	76.7	794.3	6	AX093010	Sequence
30	348	76.7	914.3	6	AX093007	Sequence
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35	348	76.7	1348.5	12	AY25220	Cloning v
36	348	76.7	14734.4	8	AC091552	Oryza sat
37	338.4	74.5	237.8	6	AR229555	Sequence
38	328.2	72.3	369.4	6	AR174859	Sequence
39	328.2	72.3	387.7	6	AR174858	Sequence
40	280.2	63.9	210.7	6	AR229556	Sequence
41	280.2	63.9	212.2	6	AR229554	Sequence
42	282.6	62.2	231.8	6	BD014494	Transgeni
43	276.6	60.9	692	6	C0834113	Sequence
44	276.6	60.9	750	6	C0834114	Sequence
45	276.6	60.9	757	6	C0834115	Sequence

## ALIGNMENTS

RESULT	1
LOCUS	A94724
DEFINITION	Sequence 2 from Patent WO934005.
ACCESSION	A94724
VERSION	A94724.1
KEYWORDS	GI:6778989
SOURCE	.
ORGANISM	unidentified unclassified unclassified
REFERENCE	1 (bases 1 to 454)
AUTHORS	Derosé,R. and Freysinet,G. MAIZE H3C4 PROMOTER ASSOCIATED WITH FIRST RICE ACTIN INTRON, CHIMERIC GENE CONTAINING IT AND TRANSFORMED PLANT Patent: WO 934005-A 2 08-JUN-1999; RHONE POULENC AGROCHIMIE (FR)
JOURNAL	Location/Qualifiers
FEATURES	location/Qualifiers
SOURCE	1..454 /organism="unidentified" /mol_type="unasigned DNA" /db_xref="taxon:32644"
ORIGIN	1..454
intron	
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Best Local Similarity	100.0%; Pired. NO. 8e-108;
Matches 454; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 GTAAACAACCCGCCCTCTCCTCTTCTCTTTCTCGTTTTTTTTTTCGTCGTCTGCAT 60
Db	1 GTAACACCCGCCCTCTCCTCTTCTCTTTCTCGTTTTTTTTTTCGTCGTCTGCAT 60
Oy	61 CTTTGCCCTTGTAAGTTGGATTGGATGGGCGAAGACGGCTTCGTGCCCAAGATCGATCGGGG 120
Db	61 CTTTGCCCTTGTAAGTTGGATTGGATGGGCGAAGACGGCTTCGTGCCCAAGATCGATCGGGG 120
Oy	121 AGGCGCGGGAATCTCGCGCATGGCTCTTCGCGGCTGAGTCGGCCCCGGAATCTCGCGGGA 180
Db	121 AGGCGCGGGAATCTCGCGCATGGCTCTTCGCGGCGTAGTCGGCCCCGGAATCTCGCGGGA 180
Oy	181 ATGGGCGCTTCGAGTGAATCTGAATCCGCGTGTGTGGGGGAATGATGGGGGCTTAA 240
Db	181 ATGGGCGCTTCGAGTGAATCTGAATCCGCGTGTGTGGGGGAATGATGGGGGCTTAA 240

Db	181	ATGGGGCCTCTGGAGTGTAGATCTGATCCGCGGTTGTTGGGGGAGATGATGGGGGCTTAA	240
Qy	241	AATTTCCGATGCTAAACAAGTACAGAAAGGGGAAAAAGGCACTATGTTTATATTTT	300
Db	241	AATTTCCGATGCTAAACAAGTACAGAAAGGGGAAAAAGGCACTATGTTTATATTTT	300
Qy	301	TATATATTTCTGCTGCTGCTGTGACGGCTTATGATGTGTAGATCTTTCTTTCTTTT	360
Db	301	TATATATTTCTGCTGCTGCTGTGACGGCTTATGATGTGTAGATCTTTCTTTCTTTT	360
Qy	361	GTGGGTAGAAATTTGAATCCTCAGCATTTTCATCGTAGTATTTTCTTTTCAATGATTTGT	420
Db	361	GTGGGTAGAAATTTGAATCCTCAGCATTTTCATCGTAGTATTTTCTTTTCAATGATTTGT	420
Qy	421	GACAAATGCAGCCTCTGTGCGGAGCTTTTGTAG	454
Db	421	GACAAATGCAGCCTCTGTGCGGAGCTTTTGTAG	454
RESULT 2			
LOCUS	AR559744	454 bp	DNA
DEFINITION	Sequence 2 from patent US 6750378.		linear
ACCESSION	AR559744		
VERSION	AR559744.1	GI:53969842	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 454)		
TITLE	Derose,R. and Freysinet,G.		
JOURNAL	Maize H3c4 promoter combined with the first intron of rice actin,		
FEATURES	chimeric gene comprising 1c and transformed plant		
	Patent: US 6750378-A 2 15-JUN-2004;		
source	Location/Qualifiers		
	1..454		
ORIGIN	/organism="unknown"		
	/mol_type="genomic DNA"		
Query Match	100.0%; Score 454;	DB 6;	Length 454;
Best Local Similarity	100.0%; Pred. No. 8e-108;		
Matches	454; Conservative	0; Mismatches	0; Indels
			Gaps 0;
Qy	1	GTAAACACCCCGCCCTCTCTCTTTCTTTCTCGTTTTTTTTTTCGTCTGCTCGAT	60
Db	1	GTAAACACCCCGCCCTCTCTCTTTCTTTCTCGTTTTTTTTTTCGTCTGCTCGAT	60
Qy	61	CTTTGGCTTGGTAATTTGGGTGGGCGAGAGCGCTTGTGCGCCAGATCGGTGGCGGG	120
Db	61	CTTTGGCTTGGTAATTTGGGTGGGCGAGAGCGCTTGTGCGCCAGATCGGTGGCGGG	120
Qy	121	AGGGGCGGGATCTCGCGGCTGGCGCTCCGGGCGTAGAGTCGGCCCGAATCCTCGGGGGA	180
Db	121	AGGGGCGGGATCTCGCGGCTGGCGCTCCGGGCGTAGAGTCGGCCCGAATCCTCGGGGGA	180
Qy	181	ATGGGCTCTCGGATGTAGATCTGATTCGCGCTTTGTTGGGGAGATGATGGGCGCTTAA	240
Db	181	ATGGGCTCTCGGATGTAGATCTGATTCGCGCTTTGTTGGGGAGATGATGGGCGCTTAA	240
Qy	241	AATTTCCGATGCTAAACAAGTACAGAAAGGGGAAAAAGGCACTATGTTTATATTTT	300
Db	241	AATTTCCGATGCTAAACAAGTACAGAAAGGGGAAAAAGGCACTATGTTTATATTTT	300
Qy	301	TATATATTTCTGCTGCTGCTGTGAGGCTTATGATGTGTAGATCTTTCTTTCTTTT	360
Db	301	TATATATTTCTGCTGCTGCTGTGAGGCTTATGATGTGTAGATCTTTCTTTCTTTT	360
Qy	361	GTGGGTAGAAATTTGAATCCTCAGCATTTTCATCGTAGTATTTTCTTTTCAATGATTTGT	420
Db	361	GTGGGTAGAAATTTGAATCCTCAGCATTTTCATCGTAGTATTTTCTTTTCAATGATTTGT	420
Qy	421	GACAAATGCAGCCTCTGTGCGGAGCTTTTGTAG	454

Db	421	GACAAATGACGCTCGTGGGAGGCTTTTGTAG	454
RESULT 3			
LOCUS	BD128390		
DEFINITION	Corn H3C4 promoter bonded to the first intron of rice actin, chimeric gene containing this promoter and transgenic plant.		
ACCESSION	BD128390.1	GI:23223335	
VERSION	JP 2002500016-A/2.		
KEYWORDS	unidentified		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 454)		
AUTHORS	Durose, R. and Freysaet, G.		
TITLE	Corn H3C4 promoter bonded to the first intron of rice actin, chimeric gene containing this promoter and transgenic plant		
JOURNAL	Patent: JP 2002500016-A 2 -JAN-2002;		
COMMENT	AVANTUS CROSCIENCE SA		
	OS Unidentified		
	PN JP 2002500016-A/2		
	PD 08-JAN-2002		
	PF 22-DEC-1998 JP 2000526660		
	PR 24-DEC-1997 FR 97/16726		
	PI RICHARD DUROSE, GEORGES FREYSAET		
	PC C12N15/09, A01H5/00, C07K14/21, C07K14/415, C07K19/00, C12N5/10, PC C12N1/68,		
	PC C12N15/00, C12N5/00		
	CC Strandedness: Single;		
	CC Topology: Linear;		
	CC Corn H3C4 promoter bonded to the first intron of rice actin,		
	CC containing this promoter and transgenic plant FH Key		
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	Location/Qualifiers	1. .454	
	1. .454	Location/Qualifiers	
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Best Local Similarity	100.0%;	Pred. No. 8e-108;	
Matches 454;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
OY	1	GTAACCAACCCGCGCCCTCTCCTCTTTCTTCTCGTATTTTTCGTCGATCGAT	60
DB	1	GTAACCAACCCGCGCCCTCTCCTCTTTCTTCTCGTATTTTTCGTCGATCGAT	60
OY	61	CTTTGGCCTTGATGTTTGGTGGGCGAGACGCGCTTCTGTCGCCAATGCGTGGG	120
DB	61	CTTTGGCCTTGATGTTTGGTGGGCGAGACGCGCTTCTGTCGCCAATGCGTGGG	120
OY	121	AGGGGCGGGATCTCGCGGCTGGGCTCCCGGGCGTGAAGCCCGATCCTCGGGGA	180
DB	121	AGGGGCGGGATCTCGCGGCTGGGCTCCCGGGCGTGAAGCCCGATCCTCGGGGA	180
OY	181	ATGGGGCTTCGATGTGATCTTGATCGCGCGTGTGTGGGGAGATGAGGGCGTTAA	240
DB	181	ATGGGGCTTCGATGTGATCTTGATCGCGCGTGTGTGGGGAGATGAGGGCGTTAA	240
OY	241	AATTTGCGCATGCTAAACAAGATAGAGAAAGGGGAAAAGGCACTATGTTTATTTT	300
DB	241	AATTTGCGCATGCTAAACAAGATAGAGAAAGGGGAAAAGGCACTATGTTTATTTT	300
OY	301	TATATTTTTCGCTGCGTCTGTCAGGCTTATGATGCTATGATCTTTCTTTCTTTT	360
DB	301	TATATTTTTCGCTGCGTCTGTCAGGCTTATGATGCTATGATCTTTCTTTCTTTT	360

QY	361	GTGGGTAAATTTGAATCCCTCAGATGTTCAATCGAGTATTTCTTTTCAATATTTGT	420
Db	361	GTGGGTAAATTTGAATCCCTCAGATGTTCAATCGAGTATTTCTTTTCAATATTTGT	420
QY	421	GACAAATGACAGCTCTGTCGGAGCTTTTGTAG	454
Db	421	GACAAATGACAGCTCTGTCGGAGCTTTTGTAG	454
RESULT 4			
LOCUS	A94725	1565 bp	DNA
DEFINITION	Sequence 3 from Patent WO934005.		linear
ACCESSION	A94725		
VERSION	A94725.1	GI:6778990	
KEYWORDS			
SOURCE	unidentified		
ORGANISM	unidentified		
REFERENCE	1 (bases 1 to 1565)		
AUTHORS	DeRose,R. and Freyrsbinet,G.		
TITLE	MAIZE H3C4 PROMOTER ASSOCIATED WITH FIRST RICE ACTIN INTRON, CHIMERIC GENE CONTAINING IT-UL-TRANSFORMED PLANT		
JOURNAL	Patent: WO 934005-A 3 08-Jul-1999;		
FEATURES	PHONE POLIENC AGROCHIMIE (FR)		
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intron	1102..1555		
ORIGIN			
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Best Local Similarity 100.0%; Pred. No. 1e-107;			
Matches 454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	GTAAACACACCCGCCCTCTCTCTTTCTTTCTCGTTTCTTTTCTGTCGTCTGCAT	60
Db	1102	GTAAACACACCCGCCCTCTCTCTTTCTTTCTCGTTTCTTTTCTGTCGTCTGCAT	1161
QY	61	CTTTGCGCTTGAGTTGGGTGGGCGAGAGCGGCTTCTGCGCCAGATCGGTGCGGG	120
Db	1162	CTTTGCGCTTGAGTTGGGTGGGCGAGAGCGGCTTCTGCGCCAGATCGGTGCGGG	1221
QY	121	AGGGCGGGGATCTCGCGGCTGCGCTCTCGGGCGAGATCGGCCCGGATCTCTCGGGGA	180
Db	1222	AGGGCGGGGATCTCGCGGCTGCGCTCTCGGGCGAGATCGGCCCGGATCTCTCGGGGA	1281
QY	181	ATGGGGCTCTCGGAGTGAATCTGATTCGCGCGTTGTGGGGGAGATGATGGGGCGTTAA	240
Db	1282	ATGGGGCTCTCGGAGTGAATCTGATTCGCGCGTTGTGGGGGAGATGATGGGGCGTTAA	1341
QY	241	AATTTGCGCATGCTAAACAGATCGAAGAGGGGAAAAAGGCACTATGTTTATATTTT	300
Db	1342	AATTTGCGCATGCTAAACAGATCGAAGAGGGGAAAAAGGCACTATGTTTATATTTT	1401
QY	301	TATATATTTTCTGCTGCTGCTGCTGATCGGCTTGAATGTGCTAATCTTTCTTTCTTTT	360
Db	1402	TATATATTTTCTGCTGCTGCTGCTGATCGGCTTGAATGTGCTAATCTTTCTTTCTTTT	1461
QY	361	GTGGGTAAATTTGAATCCCTCAGATGTTCAATCGAGTATTTCTTTTCAATATTTGT	420
Db	1462	GTGGGTAAATTTGAATCCCTCAGATGTTCAATCGAGTATTTCTTTTCAATATTTGT	1521
QY	421	GACAAATGACAGCTCTGTCGGAGCTTTTGTAG	454
Db	1522	GACAAATGACAGCTCTGTCGGAGCTTTTGTAG	1555
RESULT 5			
AR559745			

LOCUS	AR559745	1565 bp	DNA	linear	PAT 08-OCT-2004
DEFINITION	Sequence 3 from patent US 6750378.				
ACCESSION	AR559745				
VERSION	AR559745.1	GI:53969843			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 1565)				
AUTHORS	Derose,R. and Freysinet,G.				
TITLE	Maize H3C4 promoter combined with the first intron of rice actin, chimeric gene comprising it and transformed plant				
JOURNAL	Patent: US 6750378-A 3 15-JUN-2004;				
FEATURES	Location/Qualifiers				
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Query Match	100.0%;	Score 454;	DB 6;	Length 1565;	
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Db	1102	GTAACACACCCGCCCTCTCTCTTCTTCTTCGCTTTTCTTCTGCTCGCTCGAT	1161		
QY	61	CTTTGGCCTTGGTAGTTGGGTGGGCGAGAGCGGCTTCGTCGCCAGATCGGTGCGGG	120		
Db	1162	CTTTGGCCTTGGTAGTTGGGTGGGCGAGAGCGGCTTCGTCGCCAGATCGGTGCGGG	1221		
QY	121	AGGGGCGGGGATCTTCGGCGCTGCGCTTCGCCGGCTGAGTGGGCCCGGATCTCGCGGGGA	180		
Db	1222	AGGGGCGGGGATCTTCGGCGCTGCGCTTCGCCGGCTGAGTGGGCCCGGATCTCGCGGGGA	1281		
QY	181	ATGGGGCTTCGCGGATGTAGATCTGATCCGCCGTTGTTGGGGGAGATAGATGGGGCGTTAA	240		
Db	1282	ATGGGGCTTCGCGGATGTAGATCTGATCCGCCGTTGTTGGGGGAGATAGATGGGGCGTTAA	1341		
QY	241	AATTTCCGATGTCAAAACAAGATCAGAGAAGGGGAAAAGGCACTATGTTTATATTTT	300		
Db	1342	AATTTCCGATGTCAAAACAAGATCAGAGAAGGGGAAAAGGCACTATGTTTATATTTT	1401		
QY	301	TATATATTTCTGCTGCTGCTGCTGCAGGCTTAGATGTGCTAGATCTTTCCTTCTTTT	360		
Db	1402	TATATATTTCTGCTGCTGCTGCTGCAGGCTTAGATGTGCTAGATCTTTCCTTCTTTT	1461		
QY	361	GTGGGTAGAAATTGAAATCCCTCAGACATTTGTCATCGGTAGTTTTCTTTTCAAGATTGT	420		
Db	1462	GTGGGTAGAAATTGAAATCCCTCAGACATTTGTCATCGGTAGTTTTCTTTTCAAGATTGT	1521		
QY	421	GACAAATGCAGCCTCGTGGCGGAGCTTTTGTGTAG 454			
Db	1522	GACAAATGCAGCCTCGTGGCGGAGCTTTTGTGTAG 1555			
RESULT 6					
BD128391	1565 bp	DNA	linear	PAT 18-SEP-2002	
LOCUS	BD128391				
DEFINITION	Corn H3C4 promoter bonded to the first intron of rice actin, chimeric gene containing this promoter and transgenic plant.				
ACCESSION	BD128391				
VERSION	BD128391.1	GI:23223336			
KEYWORDS	JP 2002500016-A/3.				
SOURCE	unidentified				
ORGANISM	unidentified				
REFERENCE	1 (bases 1 to 1565)				
AUTHORS	Duross,R. and Freysinet,G.				
TITLE	Corn H3C4 promoter bonded to the first intron of rice actin, chimeric gene containing this promoter and transgenic plant				
JOURNAL	Patent: JP 2002500016-A 3 08-JAN-2002;				
	AVANTIS CROPS SCIENCE SA				

COMMENT	OS	Unidentified
	PN	JP 200250016-A/3
	PD	08-JAN-2002
	PF	22-DEC-1998 JP 2000526660
	PR	24-DEC-1997 FR 9716726
	PI	RICHARD DUBOSE, GEORGES PRESIDENT
	PC	C12N15/09, A01H5/00, C07K14/21, C07K14/415, C07K19/00, C12N5/10, PC C1201/68
	CC	C12N15/00, C12N5/00
	CC	Strandedness: Single;
	CC	Topology: Linear;
	CC	Corn H3c4 promoter bonded to the first intron of rice actin,
	CC	chimeric gene
	CC	containing this promoter and transgenic plant FH
	FT	Location/Qualifiers
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	FT	1..1565 Location/Qualifiers
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ORIGIN		
Query Match	100.0%; Score 454; DB 6; Length 1565;	
Best Local Similarity	100.0%; Pred. No. 1e-107;	
Matches	454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 GTAACACACCGGCCCTCTCTCTTTTCTTCGCTTTTTTTTTCGTCTGGTCTGCAT	60
DB	1102 GTAACACACCGGCCCTCTCTCTTTTCTTCGCTTTTTTTTTCGTCTGGTCTGCAT	1161
OY	61 CTTCGGCCTTGAGTAGTTGGGGGCGAGAGCGGCTTGCGCCAGATCGGATCGGCGGG	120
DB	1162 CTTCGGCCTTGAGTAGTTGGGGGCGAGAGCGGCTTGCGCCAGATCGGATCGGCGGG	1221
OY	121 AGGGCGGGGATCTCGCGGCTGCGGCTCTTCGCGGCGTGAAGTGGACCCTGCGCGGGA	180
DB	1222 AGGGCGGGGATCTCGCGGCTGCGGCTCTTCGCGGCGTGAAGTGGACCCTGCGCGGGA	1281
OY	181 ATGGGGCTCTGGGAGTAGATCTGAATCCGCCGTTTGGGGGAGAATGATGGGGGGTTAA	240
DB	1282 ATGGGGCTCTGGGAGTAGATCTGAATCCGCCGTTTGGGGGAGAATGATGGGGGGTTAA	1341
OY	241 AATTTCGCATGCTTAACAAGATCGAAGAGGGGAAAAGGCACTAATGTTTATATTTT	300
DB	1342 AATTTCGCATGCTTAACAAGATCGAAGAGGGGAAAAGGCACTAATGTTTATATTTT	1401
OY	301 TATAATTTCTGCTGCTCTGCTCATAGGCTTAGATGTGCTAATCTTTCTTTCTTTT	360
DB	1402 TATAATTTCTGCTGCTCTGCTCATAGGCTTAGATGTGCTAATCTTTCTTTCTTTT	1461
OY	361 GTGGGTAGAAATTTGAATCCCTCAGATTTGTCATGGTAGTTTTCTTTTATGATTTGT	420
DB	1462 GTGGGTAGAAATTTGAATCCCTCAGATTTGTCATGGTAGTTTTCTTTTATGATTTGT	1521
OY	421 GACAAATCGAGCTCTGTCGCGAGCTTTTGTAG	454
DB	1522 GACAAATCGAGCTCTGTCGCGAGCTTTTGTAG	1555
RESULT 7		
LOCUS	AY452735	4895 bp DNA circular SYN 19-DEC-2003
DEFINITION	Reporter vector pAcXYN,	complete sequence.
ACCESSION	AY452735	
VERSION	AY452735.1 GI:39636979	
KEYWORDS		
SOURCE	Reporter vector pAcXYN	
ORGANISM	Reporter vector pAcXYN	
REFERENCE	1 (bases 1 to 4895)	Vickers C E, Xue G P and Greenhoff P M

TITLE	A synthetic xylanase as a novel reporter in plants
JOURNAL	Plant Cell Rep. 22 (2), 135-140 (2003)
MEDLINE	22867549
PUBMED	12845475
REFERENCE	2 (bases 1 to 4895)
AUTHORS	Vickers,C.E.
TITLE	Direct Submission
JOURNAL	Submitted (29-OCT-2003) ARC Centre for Integrative Legume Research, The University of Queensland, Room 213, John Hines Building (69), St. Lucia, Qld 4072, Australia Location/Qualifiers 1..4895
FEATURES	
source	/organism="Reporter vector pActXyn" /mol_type="other DNA" /db_xref="taxon:255329"
misc_feature	267..2274 /note="sequence from cloning vector pBR322"
CDS	468..1328 /note="ampicillin resistance protein; bla" /codon_start=1 /product="beta-lactamase" /protein_id="AAP29085.1" /db_xref="GI:39636980." /translation="MSIQHPRVALIIPPAFCIPVAHPETLVKVDADQLGARVY IELDNSGKITFSRPRERPMPMSTFKVLICGVLSRIDGGQDLGRRIHSQNDLVE YSPTVEKLITDGMTFRELCSAATMTSDNTANALLTTIGAPKELTAFILNMGCHVTLL DRMEPELNEAIPLNDERDTTPVAMATTIRGLTIGELLTLASPOOLIDMDPADKVAGPL LRSLAPKGFRIADKSNGRGSRGITIAALGDPKSPRIIVITYTTSQAFTMDENRRQA EIGASLIKHW"
misc_feature	2345..2367 /note="t7 RNA polymerase promoter"
promoter	2426..3338 /note="from rice actin gene; Act1"
intron	3339..3792 /note="intron 1 from rice actin gene; Act1"
gene	3800..4513 /gene="sxyna"
CDS	3800..4513 /gene="sxyna" /note="synthetic xylanase" /codon_start=1 /product="xylanase" /protein_id="AAP29086.1" /db_xref="GI:39636981." /translation="MASNGKKFTVGNQGONQHKGNDGVSFEIWLINDTGANGSLTSGG ATPFAEWNAAVNRGNFLARRGLDFGSQKKAIDYDGLDYAAATKYTAASGNSRLCV YGMFGONGINGLPVLEYIIIEDWVDVMDQGMVITLDGOVKIFQMDHRGPITNGSS ETPCQVSNVQOKRTSGHTVSDHFEMAKQMGINGLNLYEVALNAESWGSSVADVTL LDVIYTKGSSPATSAAPR"
terminator	4535..4872
misc_feature	/note="from rbcS gene" 4895 /note="Sp6 RNA polymerase transcription initiation site"
ORIGIN	
Query Match	88.9%; Score 403.4; DB 12; Length 4895;
Best Local Similarity	98.5%; Pred. No. 2.1e-94;
Matches 450; Conservative	0; Mismatches 1; Indels 6; Gaps 4;
OY	1 GTAACCACCCCGCCCTCTCCTCTTTTCCTCGCTTTTTTTTTTGTGCTCGCTCGAT 60
Db	3339 GTAACCACCCCGCCCTCTCCTCTTTTCCTCGCTTTTTTTTTTGTGCTCGCTCGAT 3398
OY	61 CTTTGCCCTTGTAAGTTGGGTGGGCAGAGACGACTTCGTGCCCAGATCGTGCGCGG 120
Db	3399 CTTTGCCCTTGTAAGTTGGGTGGGCAGAGACGACTTCGTGCCCAGATCGTGCGCGG 3458
OY	121 AGGGGCGGGAATCTCGCGCTGAGCTTTCGGGCGTAGAGTCGACCAGATCCTCGCGGGGA 180
Db	3459 AGGGGCGGGAATCTCGCGCTGAGCTTTCGGGCGTAGAGTCGACCAGATCCTCGCGGGGA 3518
OY	181 ATGGGGCTCTCGAGTAGATCT--GATCCGCCGTTGTTGGGGAGAGATGATGGGGCTTT 238



Db	3519	ATGGGGCTCTCGAGTGTAGATCTGGGATCCGCCGTTGTTGGGGGAGATGATGGGGCGTTT	3578
Qy	229	AAAAATTT-CGCCATCTTAAACAAGATCGAGAAAGAGGGAAAAAGGCATATATGTTTATAT	297
Db	3579	AAAAATTTCCGCCATCTCTAAACAAGATCGAGAAAGAGGGAAAAAGGCATATATGTTTATAT	3638
Qy	298	TTTTATATATTTCTGCTGCTGCTCGTCAAGGCTTAGATGTGCTAGATCTTTCTTTCTCTT	357
Db	3639	TTTTATATATTTCTGCTGCTCT--TCGTCAAGGCTTAGATGTCTAGATCTTTCTTTCTCTT	3696
Qy	358	TTTGTGGGTAGAAATTTGAATCCCTCAGCATTTGTCATCGTAGATTTTCTTTTCATGAT	417
Db	3697	TTTGT-GGTAGAAATTTGAATCCCTCAGCATTTGTCATCGTAGATTTTCTTTTCATGAT	3755
Qy	418	TGTGACAAATGACGCTCTGTGGGAGCTTTTGTAG	454
Db	3756	TGTGACAAATGACGCTCTGTGGGAGCTTTTGTAG	3792
RESULT 8			
LOCUS	AX555357	470 bp	DNA
DEFINITION	Sequence 109 from Patent WO02061102.	linear	PAT 27-NOV-2002
ACCESSION	AX555357		
VERSION	AX555357.1	GI:25898876	
KEYWORDS			
SOURCE	Oryza sp.		
ORGANISM	Oryza sp.		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.		
AUTHORS	1 Paascal,E.J., Valentine,S.A., Brown,J.A., Cockrell,I.A.S. and Johnson,B.D.		
TITLE	Control of gene expression in plants		
JOURNAL	Patent: WO 02061102-A 109 08-NOV-2002;		
FEATRES	Syngenta Participations AG (CH)		
SOURCE	Location/Qualifiers		
	1..470		
ORIGIN	/organism="Oryza sp." /mol_type="unassigned DNA" /db_xref="taxon:52841"		
Query Match	84.2%; Score 382.2; DB 6; Length 470;		
Best Local Similarity	94.3%; Pred.No.4.7e-89;		
Matches	433; Conservative 0; Mismatches 13; Indels 13; Gaps 3;		
Qy	1	GTAACCAACCCGCCCTCTCTCTCTTTCTTTCTTCGCTTTTTTTTTT-CGTCTCGCTTCGA	59
Db	4	GTAACCAACCCGCCCTCTCTCTCTTTCTTTCTTCGCTTTTTTTTTTCTCGCTTCGA	63
Qy	60	TCTTTGGCTTGGATTTGGGTGGGCGAGA-----GGCGCTTCGTCCGCCAGATCGTGC	115
Db	64	TCTTTGGCTTGGATTTGGGTGGGCGAGAAGGCGGCTTCGTGCGGCCAGATCGGTGC	123
Qy	116	GCGGAGGCGGCGGATCTCGCGGCTGCGGCTTCGCGCGTGAAGTCGCGCCGATCTCGC	175
Db	124	GCGGAGGCGGCGGATCTCGCGGCT-----GGGCTCTCCCGCGGCTGAATCTCGC	175
Qy	176	GCGGAGTGGGCTCTCGGATGTGAATCTGAATCCGCCGTTGTTGGGGGAGATGATGGGCG	235
Db	176	GCGGAGTGGGCTCTCGGATGTGAATCTGAATCCGCCGTTGTTGGGGGAGATGATGGGCG	235
Qy	236	TTTAAATTTTGGCCATGTCTAAACAAGATCAGGAAGAGGGAAAAAGGCACTATGTTAT	295
Db	236	TTTAAATTTTGGCCATGTCTAAACAAGATCAGGAAGAGGGAAAAAGGCACTATGTTAT	295
Qy	296	ATTTTATATATTTCTGCTGCTGCTCGTCAAGCTTAGATGTGCTAGATCTTTCTTTCTTC	355
Db	296	ATTTTATATATTTCTGCTGCTGCTCGTCAAGCTTAGATGTGCTAGATCTTTCTTTCTTC	355
Qy	356	TTTTTTGGGTAGAAATTTGAATCCCTCAACATGTTTCATCGGATGTTTCTTTTCATGA	415

[illegible]

	DEFINITION	O. sativa Act1 gene.
	ACCESSION	X63830
	VERSION	X63830.1 GI:468505
	KEYWORDS	act1 gene; actin; Gus gene.
	SOURCE	Oryza sativa (japonica cultivar-group)
	ORGANISM	Oryza sativa (japonica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Eriatridaceae; Oryzaceae; Oryza.
	REFERENCE	1 McElroy,D., Blowers,A.D., Jenes,B. and Wu,R. Construction of expression vectors based on the rice actin 1 (Act1) 5' region for use in monocot transformation Mol. Gen. Genet. 231 (1), 150-160 (1991)
	JOURNAL	MEDLINE 92092956
	PUBMED	1753941
	REFERENCE	2 (bases 1 to 623) Wu,R.J. Direct Submission Submitted (21-MAR-1994) R.J. Wu, Cornell University, Section of Biochemistry Molecular & Cell Biology, 316 Biotechnology Building, Ithaca, NY 14853, USA
	JOURNAL	Location/Qualifiers
	FEATURES	1..623
	source	/organism="Oryza sativa (japonica cultivar-group)" /mol_type="genomic DNA" /cultivar="B-42" /sub_species="japonica" /_db_xref="taxon:39947"
	TATA_signal	1..8 join(42..120,569..623) /gene="Act1" join(42..120,569..623) /gene="Act1"
	gene	42..120 /gene="Act1" /number=1 /evidence=experimental
	mRNA	121..568 /gene="Act1" /number=1 /evidence=experimental
	exon	569..623 /gene="Act1" /number=2 /evidence=experimental
	intron	576..623 /gene="Act1" /codon_start=1 /product="actin" /protein_id="CAA45324.1" /_db_xref="GI:468506" /_db_xref="UniProt/TREMBL:Q04656" /_translation="MADAEDGSGPGGSLM"
	CDS	621..623 /gene="Gus" 621..>623 /gene="Gus" /codon_start=1 /protein_id="CAA45325.1" /_db_xref="GI:4379330" /_translation="M"
	gene	
	CDS	
	ORIGIN	
	Query Match	83.6%; Score 379.4; DB 8; Length 623;
	Best Local Similarity	93.5%; Pred. No. 2,7e-88;
	Matches	420; Conservative 0; Mismatches 21; Indels 8; Gaps 2
QY	6	CACCCGCCCTCTCTCTTTTTCCTCGTTTTTTTGCTTCGGTCTGCATCTTGG 65
Dd	128	CCCCCGCCTCTCTCTCTTTTTCCTCGTTTTTTTTCGCTCTCGTCTGCATCTTGG 187
QY	66	GCTGTGATGTTGGATGGAGAGAGCGGCTTCGTCCGACCATCGATTGGCGGAGAGGGG 125

Db	188	GCCTTGGATGTTTGGGGGCGAGAG - GCGGCTTCGTGCCCAAGATCGGTGCGCGGAGGGG	246
OY	126	CGGAGATCTCGCGGCTGCGGCTCTCCGGCGCTGAGTCCGCCCGGATCTCTGCGGGGAAATGGG	185
Db	247	CGGAGATCTCGCGGCTGGG-----GTCTCGGCGGTGCGGCGCGGATCTCTGCGGGGGAATGGG	299
OY	186	GCTCTCGGAGTGTACATCTGATCCGCGCGTGTGTGGGGGGAGATGATGGGGCGTTAAATTT	245
Db	300	GCTCTCGGATGTAGATCTGATCCGCGCTGTGTGGGGGAGATGATGGGGCGTTAAATTT	359
OY	246	CGCCATGTAAACAAGATCAGAGAAGGGGAAAAAGGCACTATGCTTATATATTTTATAT	305
Db	360	CGCCATGTAAACAAGATCAGAGAAGGGGAAAAAGGCACTATGCTTATATATTTTATAT	419
OY	306	ATTTCGTGCTGCTCGTCAGAGCTTAAATGTGCTAGATCTTTCTTTCTTTTGTGGG	365
Db	420	ATTTCGTGCTGCTCGTCAGAGCTTAAATGTGCTAGATCTTTCTTTCTTTTGTGGG	479
OY	366	TAGAATTGAATCCCTCAGCATTTGTCATCGGTATTTTCTTTCAATGATTGGACAA	425
Db	480	TAGAATTGAATCCCTCAGCATTTGTCATCGGTATTTTCTTTCAATGATTGGACAA	539
OY	426	ATGACGCTCGTGGGAGCTTTTGTAG	454
Db	540	ATGACGCTCGTGGGAGCTTTTGTAG	568

	RESULT 11				
150114	LOCUS	150114	1392 bp	DNA	linear PAT 07-OCT-1997
	DEFINITION	Sequence 6 from patent US 5641876.			
	ACCESSION	150114			
	VERSION	150114.1	GI:2472334		
	KEYWORDS	.			
SOURCE		unknown.			
ORGANISM		Unknown.			
REFERENCE		Unclassified.			
AUTHORS		1 (bases 1 to 1392)			
TITLE		McElroy,D. and Wu,R.			
JOURNAL		Rice actin gene and promoter			
FEATURES		Patent: US 5641876-A 6 24-JUN-1997;			
	source	Location/Qualifiers			
		1..1392			
		/organism="unknown"			
ORIGIN		/mol_type="unassigned DNA"			
Query Match		83.6%; Score 379.4; DB 6; Length 1392;			
Best Local Similarity		93.5%; Pred. No. 3.1e-86;			
Matches 420; Conservative		0; Mismatches 21; Indels 8; Gaps 2;			
Qy	6	CACCCCGCCCCCTCCTCTTTCCTTTCCGCCGTTTTTTTTTCGTGCAGTCGATCTTTTG	65		
Db	926	CCCCGGCGCTCTCTCTCTCTTCTTCTTCCGTTTTTTTTTTCGTGCTCGATCTTG	985		
Qy	66	GCTTGTGATGTTGGGTGGGCGAAGCGCGCTTCGTGCCCGCATCGGTGCGCGGGAAGGG	125		
Db	986	GCTTTGTGATGTTGGGGGCGAGAAG-CGGCGTTCCTCGCCAGATCGGTGCGCGGGAAGGG	1044		
Qy	126	CGGATCTCGCGGCTGGCGTCTCCGGGCGTAGTTCGGCCCGGATCTTCGCGGGAATGGG	185		
Db	1045	CGGAGATCTCGGGGCTGG-----GTCTCGGCGTGCAGCGGATCTTCGCGGGAATGGG	1097		
Qy	186	GCTCTCGGATTAATCTGATCCGCCGCTGTGGGGGAGATGGGGCGTTAAATT	245		
Db	1098	GCTCTCGGATTAATCTGATCCGCCGCTGTGGGGGAGATGGGGCGTTAAATT	1157		
Qy	246	CGCCATGCTAAACAAGATCAGAGAAGAGGCAACTATGTTTATATTATTTTATAT	305		
Db	1158	CGCCATGCTAAACAAGATCAGAGAAGGGAAGGCACTATGTTTATATTATTTTATAT	1217		
Qy	306	ATTTCGTGCTGCTCGTCAGGCTTAAGTGTAGATCTTTTCTTTCTTTTGTGGG	365		

Db	1218	ATTCTGCTGCGCTGCTGTCAGGCTTAAGATGTCATGCTTCTCTTCTTTGTGCGG	1277
Qy	366	TAGAAATTGAATCCCTCAGCAATGTTCAATCGGTAGTCTTTCTTTCAATGATTTGTGCAA	425
Db	1278	TAGAAATTGAATCCCTCAGCAATGTTCAATCGGTAGTCTTTCTTTCAATGATTTGTGCAA	1337
Qy	426	ATGCAGCCTCGGCGGAGCTTTTGTAG	454
Db	1338	ATGCAGCCTCGTGGGAGCTTTTGTAG	1366
RESULT 12			
LOCUS	150115	1404 bp	DNA
DEFINITION	Sequence 7 from patent US 5641876.	linear	PAT 07-OCT-1997
ACCESSION	150115		
VERSION	150115.1		GI:2472335
KEYWORDS			
SOURCE	.		
ORGANISM	unknown.		
REFERENCE	1 (bases 1 to 1404)		
AUTHORS	McIlroy,D. and Wu,R.		
TITLE	Rice actin gene and promoter		
JOURNAL	Patent: US 5641876-A 7 24-JUN-1997;		
FEATURES	Location/Qualifiers		
source	1..1404		
	/organism="unknown"		
ORIGIN	/mol_type="unassigned DNA"		
Query Match	83.6%; Score 379.4; DB 6; Length 1404;		
Best Local Similarity	93.5%; Pred. No. 3.1e-88;		
Matches	420; Conservative 0; Mismatches 21; Indels 8; Gaps 2;		
Qy	6	CACCCGCGCCCTCTCTCTCTTCTTCTCCGTTTCTTTTGTGCTCGGTCGATCTTGG	65
Db	936	CCCCGCGCCCTCTCTCTCTTCTCCGTTTCTTTTGTGCTCGGTCGATCTTGG	995
Qy	66	GCCTTGTAGTTTGGGTGGGAGAGCGGAGCTTCGCGCCAGATCGGCGCGGGAGGG	125
Db	996	GCTTGTAGTTTGGGGGGAGAG-GCGGCTTCGTCGCCAGATCGGTGCGGGAGGG	1054
Qy	126	CGGAGTCTCGGGGCTGCGGCTCCGGGCGTAGTCGCGCCGATCTCGCGGGAGATGG	185
Db	1055	CGGAGTCTCGGGGCTG-----GTCGCGGTGCGGCGGATCTCGCGGGAGATGG	1107
Qy	186	GCTCTCGATAGATCTGATTCGCGCTGTTGGGGAGATGATGGGCGTTTAAATT	245
Db	1108	GCTCTCGATAGATCTGATTCGCGCTGTTGGGGAGATGATGGGCGTTTAAATT	1167
Qy	246	CGCCATGCTAAACAAGATCAGAGAAAGGGGAAAGGCACTATGTTATAATTTTAT	305
Db	1168	CGCCATGCTAAACAAGATCAGAGAAAGGGGAAAGGCACTATGTTATAATTTTAT	1227
Qy	306	ATTCTGCTGCTGCTGCTGCTAGGCTTAAATGCTAGATCTTCTCTTTTGTGGG	365
Db	1228	ATTCTGCTGCTGCTGCTGCTAGGCTTAAATGCTAGATCTTCTCTTTTGTGGG	1287
Qy	366	TAGAAATTGAATCCCTCAGCAATGTTCAATCGGTAGTCTTTCTTTCAATGATTTGTGCAA	425
Db	1288	TAGAAATTGAATCCCTCAGCAATGTTCAATCGGTAGTCTTTCTTTCAATGATTTGTGCAA	1347
Qy	426	ATGCAGCCTCGGCGGAGCTTTTGTAG	454
Db	1348	ATGCAGCCTCGTGGAGCTTTTGTAG	1376
RESULT 13			
LOCUS	150113	2199 bp	DNA
DEFINITION	Sequence 5 from patent US 5641876.	linear	PAT 07-OCT-1997
ACCESSION	150113		

VERSION	150113.1	GI:2472333
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified.	
AUTHORS	1 (bases 1 to 2199)	
TITLE	McElroy, D. and Wu, R.	
JOURNAL	Rice actin gene and promoter	
FEATURES	Patent: US 5641876-A 5 24-JUN-1997;	
source	Location/Qualifiers	
	1..2199	
	/organism="unknown"	
ORIGIN	/mol_type="unassigned DNA"	
Query Match	83.6%;	Score 379.4; DB 6; Length 2199;
Best Local Similarity	93.5%;	Pred. No. 3,4e-88;
Matches 420;	Conservative 0;	Mismatches 21; Indels 8; Gaps 2;
QY	6	CACCCGCCCCCTCTCCCTCTTCTTCTTCGCTTTTTCGTCGCTCCGATCTTTTG 65
DB	1733	CCCCGCGCTCCCTCCCTCTTCTTCTTCGCTTTTTCGCTCGCTCGATCTTTTG 17922
QY	66	GCCCTGGTAGTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 125
DB	1793	GCCCTGGTAGTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1851
QY	126	CGGAGATCGCGCGCTGCGCTCTCCGCGCGCTGAGTCGCGCCGATCTCGCGGAGATGG 185
DB	1852	CGGAGATCTCCGCGCTG-----GTCTCGGCGTGGCGCGGAGATCCGCGGAGATGG 1904
QY	186	GCTCTCGGAGTAGATGTGATCCGCGCTGTGTGGGGAGATGATGGGCGTTAAAAATT 245
DB	1905	GCTCTCGGAGTAGATCTGATCCGCGCTGTGTGGGGAGATGATGGGCGTTAAAAATT 1964
QY	246	CGCATCTTAAACAAGATCAGAAAGAGGGAAGGCACTAAGGTTATATTTTATAT 305
DB	1965	CGCATCTTAAACAAGATCAGAAAGAGGGAAGGCACTAAGGTTATATTTTATAT 2024
QY	306	ATTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 365
DB	2025	ATTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2084
QY	366	TAGATTTGAATCCCTCAGCATTTGTTTCATGTTTCTTTTCATGATTTGACAA 425
DB	2085	TAGATTTGAATCCCTCAGCATTTGTTTCATGTTTCTTTTCATGATTTGACAA 2144
QY	426	ATGCAGCCTGTGTGGAGCTTTTGTAG 454
DB	2145	ATGCAGCCTGTGTGGAGCTTTTGTAG 2173
RESULT 14		
LOCUS	150112	5643 bp DNA linear PAT 07-OCT-1997
DEFINITION	Sequence 4 from patent US 5641876.	
ACCESSION	150112	
VERSION	150112.1	GI:2472332
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified.	
AUTHORS	1 (bases 1 to 5643)	
TITLE	McElroy, D. and Wu, R.	
JOURNAL	Rice actin gene and promoter	
FEATURES	Patent: US 5641876-A 4 24-JUN-1997;	
source	Location/Qualifiers	
	1..5643	
	/organism="unknown"	
ORIGIN	/mol_type="unassigned DNA"	
Query Match	83.6%;	Score 379.4; DB 6; Length 5643;



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Run on: September 11, 2005, 22:00:56 ; Search time 194.282 Seconds  
(without alignments)  
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Title: US-10-758-799-2

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Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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3: geneseqn20008:\*  
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6: geneseqn20028:\*  
7: geneseqn20028:\*  
8: geneseqn20038:\*  
9: geneseqn20038:\*  
10: geneseqn20038:\*  
11: geneseqn20048:\*  
12: geneseqn20048:\*  
13: geneseqn20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	454	100.0	454	AAZ91038	Aaz91038 Rice acti
2	454	100.0	1565	AAZ91039	Aaz91039 Chimeric
3	402.4	88.6	13680	ADP73931	Adp73931 Plasmid P
4	382.2	84.2	470	ABT07357	Abt07357 Reporter
5	382.2	84.2	470	ADP49181	Adp49181 Rice acti
6	379.4	83.6	623	AAZ47117	Aaz47117 Rice acti
7	379.4	83.6	623	ABK86738	Abk86738 Rice acti
8	379.4	83.6	1392	AAH80053	Aah80053 Rice acti
9	379.4	83.6	2199	AAH80052	Aah80052 Rice acti
10	379.4	83.6	5643	AAH80055	Aah80055 Rice acti
11	357.4	78.7	9359	ABK11039	Abk11039 pVDH636 v
12	357.4	78.7	9359	ABK10687	Abk10687 Transform
13	355.8	78.4	491	AAZ51179	Aaz51179 Intron of
14	355.8	78.4	491	ACA05324	Aca05324 Rice acti
15	355.8	78.4	3039	AAZ51644	Aaz51644 Bacillus
16	355.8	78.4	3039	AAZ51645	Aaz51645 Bacillus
17	355.8	78.4	3039	AAZ51793	Aaz51793 Bt.cry3Bb
18	355.8	78.4	3039	AAZ51792	Aaz51792 Bt.cry3Bb
19	355.8	78.4	3039	ABX95189	Abx95189 B. thuring
20	355.8	78.4	3039	ABX95188	Abx95188 B. thuring

21	355.8	78.4	3044	AAZ51656	Aaz51656 Bacillus
22	355.8	78.4	3044	AAZ51657	Aaz51657 Bt.cry3Bb
23	355.8	78.4	3044	ABX95200	Abx95200 B. thuring
24	355.8	78.4	3450	AAZ51643	Aaz51643 Bacillus
25	355.8	78.4	3450	AAZ51644	Aaz51644 Bt.cry3Bb
26	355.8	78.4	3450	AAZ51645	Aaz51645 Bt.cry3Bb
27	355.8	78.4	3455	AAZ51655	Aaz51655 Bacillus
28	355.8	78.4	3455	AAZ51656	Aaz51656 Bt.cry3Bb
29	355.8	78.4	3455	ABX95189	Abx95189 B. thuring
30	355.8	78.4	3469	AAZ51646	Aaz51646 Bacillus
31	355.8	78.4	3469	AAZ51647	Aaz51647 Bt.cry3Bb
32	355.8	78.4	3469	ABX95190	Abx95190 B. thuring
33	355.8	78.4	5170	ADK98488	Adk98488 B. thuring
34	355.8	78.4	5600	ADK98490	Adk98490 B. thuring
35	348	76.7	4032	AAZ23237	Aaz23237 Plasmid P
36	348	76.7	5118	ADP73930	Adp73930 Plasmid P
37	348	76.7	6865	AAH80287	Aah80287 Nucleotid
38	348	76.7	7545	ACF58343	Acf58343 Nucleotid
39	348	76.7	7943	AAH80289	Aah80289 Nucleotid
40	348	76.7	9143	AAH80286	Aah80286 Nucleotid
41	348	76.7	10003	AAH80295	Aah80295 Nucleotid
42	348	76.7	10003	AAH80295	Aah80295 Nucleotid
43	348	76.7	11643	ACF58344	Acf58344 Nucleotid
44	340.8	75.1	2181	ADK84543	Adk84543 Rice acti
45	338.4	74.5	2378	AAZ01016	Aaz01016 Expressio

## ALIGNMENTS

RESULT 1	
AAZ91038	AAZ91038 standard; DNA; 454 BP.
XX	XX
AC	AAZ91038;
XX	XX
DT	06-JUN-2000 (first entry)
XX	XX
DE	Rice actin gene intron 1 sequence.
XX	XX
KM	Regulatory element; monocotyledonous vegetable plant cell; maize;
KW	histone H3c4; promoter; rice actin gene intron; chimeric; ss;
KM	herbicide resistance.
XX	XX
OS	Oryza sativa.
XX	XX
PN	FR2727287-A1.
XX	XX
PD	25-JUN-1999.
XX	XX
PF	24-DEC-1997; 97FR-00016726.
XX	XX
PR	24-DEC-1997; 97FR-00016726.
XX	XX
PA	(RHON ) RHONE-POULENC AGROCHIMIE.
XX	XX
PI	Derose R, Freysinet G;
XX	XX
DR	WPI; 1999-397352/34.
PT	5' chimeric regulatory region comprising maize histone H3c4 promoter and
XX	rice actin gene first intron.
PS	Claim 5; Page 14; 24pp; French.
CC	The invention relates to a DNA sequence (AAZ91039) comprising a 5'
CC	regulatory element for the expression of a heterologous gene in a
CC	monocotyledonous vegetable plant cell. The DNA comprises: (a) a
CC	functional fragment of the maize histone H3c4 promoter sequence
CC	(AAZ91037); and (b) a functional fragment of the first intron of the rice
CC	actin gene (this sequence). The chimeric regulatory region is useful for
CC	the expression of heterologous genes that confer resistance to certain
CC	herbicides, or that have novel agronomical properties in monocotyledons.



	Transgenic plant; immunoglobulin production; recombinant production; glycosylation; fucose; glycan; virulence; immunotherapy; maize; gamma-zein promoter; rice; actin promoter; phosphinothricin acyltransferase; PAT; mouse; leader sequence; herpes simplex virus; HSV1; HSV2; human; monoclonal antibody HX8; Iga; heavy chain; light chain; codon optimised; plaemid; pDAB9505; cyclic; cticular; de.
XX	Zea mays.
OS	Mus sp.
OS	Homo sapiens.
OS	Oryza sativa.
OS	Chimeric.
OS	Synthetic.
OS	Unidentified.
XX	
FT	Key
FT	misc_feature
FT	Location/Qualifiers
FT	424..1589
FT	/tag= a
FT	/label= SAR
FT	/note= "Scaffold attachment region. Also referred to as MAR (matrix association region)"
FT	1673..3175
FT	/tag= b
FT	/note= "Maize gamma-zein promoter"
FT	3178..4671
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FT	/product= "Heavy chain of human anti-HSV1/HSV2 monoclonal IgG antibody HX8 (with mouse leader sequence)"
FT	3178..3234
FT	/tag= c
FT	/note= "Mouse leader sequence"
FT	3235..4668
FT	/tag= e
FT	/product= "Mature HX8 heavy chain"
FT	4678..5045
FT	/tag= f
FT	/note= "Maize pers 3'UTR"
FT	5157..6659
FT	/tag= g
FT	/note= "Maize gamma-zein promoter"
FT	6662..7363
FT	/tag= i
FT	/product= "Heavy chain of human anti-HSV1/HSV2 monoclonal IgA antibody HX8 (with mouse leader sequence)"
FT	6662..6778
FT	/tag= h
FT	/note= "Mouse leader sequence"
FT	6719..7360
FT	/tag= j
FT	/product= "Mature HX8 heavy chain"
FT	7370..7737
FT	/tag= k
FT	/note= "Maize pers 3'UTR"
FT	7889..9258
FT	/tag= l
FT	/note= "Rice actin promoter/intron"
FT	9261..9815
FT	/tag= m
FT	/product= "Phosphinothricin acyltransferase (PAT)"
FT	/note= "The PAT coding region is given in the specification as positions 9260-9820"
FT	9831..10162
FT	/tag= n
FT	/note= "Maize lipase 3'UTR"
FT	10229..11394
FT	/tag= o
FT	/label= SAR
FT	/note= "Scaffold attachment region. Also referred to as MAR (matrix association region)"
XX	
PX	W02004050838-A2.

XD		17-JUN-2004.
PD		
PF	28-NOV-2003;	2003MO-US037905.
XX		
PR	27-NOV-2002;	2002US-0429385P.
PA	(DOMC ) DOM CHEM CO.	
PA	(DOMC) DOM AGROSCIENCES LLC.	
PA	(EPIC-) EPICYTE PHARM INC.	
XX		
P1	Briggs K, Glancy T, Hein MB, Hiatt AC, Karnoup AL, Anderson WHK;	
P1	Parredy D, Petrolino J, Rubin-Wilson B, Taylor D, Roberts UJ,	
XX		
DR	WPI, 2004-461111/43.	
PT	P-PDSB; ADP73848, ADP73856.	
PT		
PT	Novel plant-produced immunoglobulin having glycopeptide or glycan profile	
PT	infection.	
PS	Claim 69; SEQ ID NO 85; 212pp; English.	
CC	The invention relates to the production of immunoglobulins in plants,	
CC	wherein at least a portion of the glycans attached to the immunoglobulins	
CC	lack fucose. The immunoglobulins produced can be of any class (i.e., IgG,	
CC	IgA, IgM, IgE or IgD) and especially an anti-herpes simplex virus	
CC	(HSV) antibody or an anti-alphaHerpes3, alphaHerpes dual integrin	
CC	antibody. The invention also relates to constructs, plasmids and vectors	
CC	for producing the immunoglobulins; transformed plant cells, calli, plant	
CC	tissues and whole plants for producing the immunoglobulins; methods for	
CC	producing the immunoglobulins, the immunoglobulins thus produced; and the	
CC	use of such immunoglobulins. The immunoglobulins of the invention may be	
CC	used to treat HSV infection or tumour angiogenesis. The invention	
CC	provides the advantages of antibody production in plants, such as large	
CC	scale production, reduced costs, and elimination of pathogenic	
CC	contaminants such as viruses and prions, with a simplified (i.e., non-	
CC	plant-specific) glycosylation profile which reduces the risk that the	
CC	immunoglobulin may not be functional in animals. The present sequence	
CC	represents the plasmid pDAB8505, which contains codon optimised DNA	
CC	sequences encoding the heavy and light chains of the human anti-HSV1/HSV2	
CC	monoclonal IgA antibody HX8 each of which are fused to mouse leader	
CC	sequences. Both heavy and light chain fusion genes are under the control	
CC	of maize endosperm-specific gamma-zein promoters. The plasmid also	
CC	contains a phosphomucinacin acyltransferase (PAT) gene under the control	
CC	of a rice actin promoter.	
SQ	Sequence 13680 BP; 3886 A; 3069 C; 2934 G; 3788 T; 0 U; 3 Other;	
	Query Match 88.6%; Score 402.4; DB 12; Length 13680;	
	Best Local Similarity 98.0%; Pred. No. 5.3e-104;	
	Matches 451; Conservative 0; Mismatches 1; Indels 8; Gaps 4	
OY	1 GTTACCAAGCCCCCTCTCTCTTTCTTCGCTTTTTTTTGCTCGGTCTGGAT 60	
DB	8796 GTTAACCAAGCCCCCTCTCTCTTTCTTCGCTTTTTTTTGCTCGGTCTGGAT 8855	
OY	61 CTTTGGCCTTAGATTGGATGGAGGCAGAGAGCGCTTGTCGCCACAGTCGGTCCGGG 120	
DB	8856 CTTTGGCCTTAGATTGGATGGAGGCAGAGAGCGCTTGTCGCCACAGTCGGTCCGGG 8910	
OY	121 AGGAGGCGGGATCTCGCGCGCTGCCTCCGGGCGGTGAATCGGCCGAGTCTCGCGGGGA 1800	
DB	8916 AGGAGGCGGGATCTCGCGCGCTGCCTCCGGGCGGTGAATCGGCCGAGTCTCGCGGGGA 8977	
OY	181 ATGGGCGCTCTCGGATGTAAATCT--GATCCGCGCTGTGGGGGAGATGATGGGCGCTT 238	
DB	8976 ATGGGCGCTCTCGGATGTAAATCTCGGATCCGCGCTGTGGGGGAGATGATGGGCGGCTT 9033	
OY	239 AAAAATTT-GCCCATGTCAAACAAGATACAGAAAGAGGGGAAAAGGGCACATAATGTTTAT 2977	
DB	9036 AAAAATTTCCGCATGTCAAACAAGATACAGAAAGAGGGGAAAAGGGCACATAATGTTTAT 9099	
OY	298 TTATATATATTTCTGCTGCTGCTCGACGCTTAGATGTGCTAGA---TCTTCTTTCTT 3544	



Db	9096	TTTATATATTTCGCTCT--TCGTACGGCTTGATGTGCTAGATCTTCTTTCTTTCTT	9153
Oy	355	CTTTTGTGGGAGAAITTTGAATCCCTCAGCATTTGTCATCGTAGTTTTCTTTTCATG	414
Db	9154	CTTTTGTGGGAGAAITTTGAATCCCTCAGCATTTGTCATCGTAGTTTTCTTTTCATG	9213
Oy	415	ATTGTGCACAATGCAAGCTCTGTGGGAGCTTTTTTTGAG	454
Db	9214	ATTGTGCACAATGCAAGCTCTGTGGGAGCTTTTTTTGAG	9253

RESULT 4  
ABT07357  
ID ABT07357 standard; DNA; 470 BP.

DT 07-NOV-2002 (first entry)

Reporter construct rice actin intron SEQ ID NO: 109.

KW Plant; gene expression control; insect; hormone receptor; fertility;  
KW ecdysone receptor; ds.

*Oryza sativa.*

PN WO200261102-A2.

PD 08-AUG-2002.

PF 24-OCT-2001; 2001WO-US051417.

PR 24-OCT-2000; 2000US-0242969P.

PA (SYGN ) SYNGENTA PARTICIPATIONS AG.

PI pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;

DR WPI; 2002-619259/66.

PT New receptor cassette encoding a chimeric receptor polypeptide, useful in  
PT regulating expression of target polypeptides in plants in the presence of  
PT appropriate ligands that may be used in controlling plant fertility.

PS Example 10; Page 263; 319pp; English.

The present invention relates to a receptor cassette encoding a chimeric receptor polypeptide comprising at least one DNA binding domain, a hinge domain of an ecdysone receptor (EcR) of an insect, a ligand binding domain of an insect RGF, where the ligand binding domain is heterologous with respect to the hinge domain and an activation domain. The chimeric insect hormone receptors and receptor cassettes are useful in regulating expression of target polypeptides in plants in the presence of appropriate ligands that may be used in controlling plant fertility. The method is useful for decreasing or increasing plant gene expression. The present sequence is a polynucleotide described in the exemplification of the invention

Sequence 470 BP; 75 A; 103 C; 141 G; 151 T; 0 U; 0 Other;

Query Match 84.2%; Score 382.2; DB 6; Length 470;

Matches 433; Conservative 0; Mismatches 13; Indels 13; Gaps 3;

QY 1 GTACCACCCCGCCCTCTCTTCTTCTTCTCCGTTT TTTT - CGTCGCGTCTCGA 59

Db 4 GTACCAACCCGCCCTCTCTTCTTCTTCTCCGTTTCTTCTCCGTCCTCGGTCGA 63

60 TCTTGGCCTTGGTAGTTGGGTGGCGAGA---GCGGCTTCGTCGCCCAGATCGGTGC 11

Db 64 TCCTTGGCCTTGGTAGTTTGGGTGGCGAGAGCGCGCTTCGTGCGCGCCAGATCGGTGC 12

[illegible]

RESULT 5  
ADDF49181  
ID ADDF49181 standard; DNA; 470 BP

AC ADF49181;

DT 12-FEB-2004 (first entry)

DE Rice actin intron.

KW receptor cassette; chimeric receptor polypeptide; DNA binding domain;

KW activation domain; transgenic seed; transgenic plant; plant line;

XX

05 Oryza sp.

PN US2003154509-A1.

PD 14-AUG-2003.

PF 24-OCT-2001; 2001US-00087167

PR 24-OCT-2001; 2001US-00087167

PA (PASC/) PASCAL E J.

PA (BROW/) BROWN J A.

PA (JOHN/) JOHNSON B D.

PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;

DR WPI; 2003-897756/82.

PT New receptor cassette encoding a chimeric receptor polypeptide, useful

PT presence of appropriate chemical ligands.

PS Example 10; SEQ ID NO 109; 186bp; English

The invention describes a receptor cassette encoding a chimeric receptor polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge (D) domain of an edg-type receptor (EDR) of an insect, a ligand binding (E) domain that is heterologous with respect to the D domain, and an activation domain. The receptor cassette and method are useful in regulating the expression of target polypeptides in plants in the presence of appropriate chemical ligands. The transgenic seeds and plants



Oy	306	ATTTCGTGCTGCTGCTGCTGCTGCTAGAGTGTGTAGATCTTTCTTTCTTTCTTTGTGGG	365
Db	420	ATTTCGTGCTGCTGCTGCTGCTAGAGCTTAGATGCTTACATCTTTCTTTCTTTGTGGG	479
Oy	366	TAGAATTGGAATCCCTCAGCATTTGTCATCGGAGATTTTCTTTTCATATTTGTGACAA	425
Db	480	TAGAATTGGAATCCCTCAGCATTTGTCATCGGAGATTTTCTTTTCATATTTGTGACAA	539
Oy	426	ATGCAGCCTCGTGGCGAGCTTTTTTGTAG	454
Db	540	ATGCAGCCTCGTGGCGAGCTTTTTTGTAG	568
RESULT 7			
ABK86738			
ID	ABK86738 standard; DNA; 623 BP.		
AC	ABK86738;		
XX			
DT	24-SEP-2002 (first entry)		
XX			
DE	Rice Act1 gene.		
XX			
KW	Rice; gene; ds; transgenic; plant; lignocellulose; cellulase; ligninase;		
KW	fermentable sugar; ethanol; fermentation; silage; feed; fuel;		
KW	industrial chemical; biodegradation; chloroaromatic;		
KM	environmental pollutant; Act1.		
OS	Oryza sativa.		
PN	WO200234926-A2.		
XX			
PD	02-MAY-2002.		
XX			
PF	18-OCT-2001; 2001WO-US032538.		
XX			
PR	20-OCT-2000; 2000US-0242408P.		
XX			
PA	(UNMS ) UNIV MICHIGAN STATE.		
PI	Sticklen MB, Dale BE, Macpool S,		
DR	WPI; 2002-489947/52.		
XX			
PT	Producing transgenic plants which after harvest degrade lignin and		
PT	cellulose to fermentable sugars, by mating transgenic plant comprising		
PT	DNA encoding cellulase with transgenic plant comprising DNA encoding		
PT	ligninase.		
PS	Example 1; Page 124; 126pp; English.		
XX			
CC	The invention discloses the production of a transgenic plant which		
CC	degrades lignocellulose when the plant is ground. It comprises the		
CC	production of the transgenic plant including cellulase and ligninase by		
CC	mating a transgenic plant, containing a DNA encoding a cellulase, and a		
CC	transgenic plant, containing a DNA encoding a ligninase, where both genes		
CC	are operably linked to a nucleotide sequence encoding a signal peptide		
CC	which targets the fusion protein to an organelle of the plant,		
CC	particularly chloroplasts. The method is useful for producing a		
CC	transgenic plant (e.g. maize) which degrades lignocellulose when the		
CC	plant is ground to produce a plant material. This material is useful for		
CC	converting lignocellulose, in a plant material, to fermentable sugars		
CC	which are then fermented to ethanol. The transgenic plants also provide a		
CC	plentiful and inexpensive source of fungal or bacterial cellulases and		
CC	ligninases which can be used in the production of ethanol. They can also		
CC	be used for pre-treating silage to increase the energy value of		
CC	lignocellulosic feeds for cows and other ruminant animals, pre-treating		
CC	lignocellulosic biomass for fermentative conversion to fuels and		
CC	industrial chemicals, and biodegradation of chloroaromatic environmental		
CC	pollutants. The sequence presented is the rice Act1 gene and promoter		
XX			
SO	Sequence 623 BP; 98 A; 184 C; 164 G; 177 T; 0 U; 0 Other;		

	Query Match	83.6%	Score 379.4	DB 6	Length 623:
	Best Local Similarity	93.5%	Pred. No.5.4e-98;		
	Matches 420:	Conservative 0;	Mismatches 21;	Indels 8;	Gaps 2
QY	6	CACCCGCGCCTCTCTCTTCTTTCTTCGTTTTTTTTTGCTCGTCCGGTTCGATCTTTG	65		
Db	128	CCCCGCAGTCCCTCTCTCTTCTTTCTTCGATTTTTTTCGATCAGCTCTGAATCTTTG	187		
QY	66	GCTTTGTGATTTTGGGTGGGAGAAGCGGCTTCGTCCGCCAGATGGGTGGCGGGAGGGG	125		
Db	188	GCTTTGTGATTTTGGGAGGAGAG-GCGGCTTCGTCCGCCAGATGGGTGGCGGGAGGGG	246		
QY	126	CGGATCTCGGCGCTGGCGGTCTCCGGGCGTAGTCCGCCGATCCTCGCGGAATGGG	185		
Db	247	CGGATCTCGGCGGTG-----GTCTCCGGGTCCGCCGATCCTCGCGGAATGGG	299		
QY	186	GCTCTCGGATGTAAATCTGAATCCGCCCTTTGTGGGGAGAGATNCGGCGCTTAATAATT	245		
Db	300	GCTCTCGGATGTAAATCTGAATCCGCCCTTTGTGGGGAGAGATNCGGCGCTTAATAATT	359		
QY	246	CGCATGTAAACAAGATCAGAGAAGGGGAAAAGGCGACTATGTTTATATTTTATAT	305		
Db	360	CGCATGTAAACAAGATCAGAGAAGGGGAAAAGGCGACTATGTTTATATTTTATAT	419		
QY	306	ATTTCGTGCTGCTCGTCAGGCTTAATGTGCTAATCTTTCTTTCTTTTGTGGG	365		
Db	420	ATTTCGTGCTGCTCGTCAGGCTTAATGTGCTAATCTTTCTTTCTTTTGTGGG	479		
QY	366	TAGAATTTGAATCCCTCAGCATGTTCAACGGIATTTTTCTTTTCATGATTTGTACA	425		
Db	480	TAGAATTTGAATCCCTCAGCATGTTCAACGGIATTTTTCTTTTCATGATTTGTACA	539		
QY	426	ATGCAGCCTCGTCCGAGCTTTTTTTGAG	454		
Db	540	ATGCAGCCTCGTCCGAGCTTTTTTTTGTGAG	568		

RESULT 8	
AA80053	
ID	AA80053 standard; cDNA; 1392 BP.
XX	
AC	AA80053;
XX	
DT	25-MAR-2003 (revised)
DT	04-NOV-1997 (first entry)
XX	
DE	Rice actin 1 gene promoter fragment.
XX	
KW	Promoter; rice; actin 1 gene; cytoplasm; cytoskeleton; extension growth
KW	cytoplasmic streaming; cell division; Rac1, maize; Adh1 promoter; ss.
XX	
OS	Oryza sativa.
XX	
PN	US5641876-A.
XX	
PD	24-JUN-1997.
XX	
PF	27-OCT-1993; 93US-00144602.
XX	
PR	05-JAN-1990; 90US-00461490.
PR	18-SEP-1991; 91US-00762680.
XX	
PA	(CORR ) CORNELL RES FOUND INC.
XX	
PI	Wu R, Mcelroy D;
XX	
DR	WPI; 1997-340996/31.
XX	
PT	Nucleic acid containing the promoter of the rice actin-1 gene - used to
PT	direct efficient expression of foreign genes in rice.
XX	
PS	Claim 4; Col 35-38; 29pp; English.
XX	















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OM nucleic - nucleic search, using sw model

Run on: September 11, 2005, 23:36:11 ; Search time 1190.88 Seconds  
(without alignments)  
14511.284 Million cell updates/sec

Title: US-10-758-799-2

Perfect score: 454  
Sequence: 1 GTTACACACCCGCCCTCTC.....CGTCCGAGCTTTTGTAG 454

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 segs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hlc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gsb1:\*  
9: gb\_gsb2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	116.4	25.6	542	5	BQ609717 BRY_5803
2	53.2	11.7	922	9	CNS0073W AL066784 Drosophi1
3	53.2	11.7	1083	9	AG429940 Mus muscu
4	52.8	11.6	1013	9	AL106871 Drosophi1
5	51.8	11.4	895	9	CNS0071A AL066286 Drosophi1
6	51.6	11.4	884	9	CNS006U0 AL065923 Drosophi1
7	51.2	11.3	919	9	CNS006S5 AL065856 Drosophi1
8	50	11.0	686	8	BZ031798 oel99D01
9	49.4	10.9	789	9	B1886452 ZF637-1-0
10	48.6	10.7	909	9	CNS00JTL AL076720 Drosophi1
11	47.6	10.5	1036	9	CNS010BS AL098770 Drosophi1
12	47.6	10.5	1656	9	CL496209 SATL_620
13	46.2	10.2	822	9	CNS009CW AL053618 Drosophi1
14	46	10.1	1101	9	AL108460 Drosophi1
15	45.6	10.0	602	7	CV131848 L3P0904
16	45.4	10.0	718	9	AG605189 Mus muscu
17	45.2	10.0	951	8	AZ672893 ENTJ74TF
18	44.5	9.9	1101	9	CNS00397 AL063912 Drosophi1
19	44.6	9.8	335	4	B1849271 476584 WA
20	44.6	9.8	889	9	CL484887 SATL_404
21	44.2	9.7	1244	9	AG390554 Mus muscu
22	44	9.7	836	9	AG390594 Mus muscu
23	44	9.7	1100	9	CNS00G3S AL071398 Drosophi1
24	44	9.7	1101	9	CNS00BNG AL057398 Drosophi1

C	25	43.6	9.6	827	6	CB945739	CB945739
C	26	43.6	9.6	1083	4	BC786263	BC786263
C	27	43.6	9.6	1101	9	CNS014Y2	AL104756 Drosophi1
C	28	43	9.5	658	9	CNS06V94	AL16846 T7 end of
C	29	43	9.5	727	9	AG122958	AG122958 Pan trogl
C	30	43	9.5	1151	9	CNS024YU	AL161216 Tetradon
C	31	42.8	9.4	995	5	BO876303	BO876303 AGENCOURT
C	32	42.8	9.4	1003	1	AL569374	AL569374
C	33	42.8	9.4	1101	9	CNS00H28	AL074533 Drosophi1
C	34	42.8	9.4	1130	9	AG176166	AG176166 Pan trogl
C	35	42.6	9.4	583	5	BP316620	BP316620 BP316620
C	36	42.4	9.3	181	2	AM449874	AM449874 UI-H-B13
C	37	42.4	9.3	384	7	CF098527	CF098527 ORN7011.Y
C	38	42.4	9.3	634	8	AZ574188	AZ574188 325Pvg12
C	39	42.4	9.3	715	9	CL598191	CL598191 OB_Ba006
C	40	42.4	9.3	747	9	AG514518	AG514518 Mus muscu
C	41	42.4	9.3	842	9	CNS0234R	AL179244 Tetradon
C	42	42.4	9.3	987	9	CNS004EE	AL051333 Drosophi1
C	43	42.4	9.3	1101	9	CNS0170G	AL108298 Drosophi1
C	44	42.4	9.3	1209	9	CL486043	CL486043 SATL_426
C	45	42.2	9.3	864	9	AG141680	AG141680 Pan Trogl

#### ALIGNMENTS

RESULT 1  
LOCUS BQ609717 542 bp mRNA linear EST 25-JUN-2002  
DEFINITION BRY 5803 wheat EST endosperm library Triticum aestivum cDNA 5',  
mRNA sequence.  
ACCESSION BQ609717 GI:21559056  
VERSION BQ609717  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum

REFERENCE  
AUTHORS Clarke,B., Lambrecht,M. and Rhee,S.Y.  
TITLE Arabidopsis genomic information for interpreting wheat EST  
sequences  
1 (bases 1 to 542)  
JOURNAL Arabidopsis genomic information for interpreting wheat EST  
MEDLINE  
PUBMED  
Funct. Integr. Genomics 3 (1-2), 33-38 (2003)

COMMENT  
Contact: Lambrecht M  
The Arabidopsis Information Resource  
Carnegie Institution of Washington, Dept. of Plant Biology  
260 Panama Street, Stanford, CA 94305, USA  
Tel: 1 650 325 1521 x 251  
Fax: 1 650 325 3748  
Email: rhee@acoma.stanford.edu.  
Location/Qualifiers

#### FEATURES

Source  
1..542  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultivar="WYuna"  
/db\_xref="taxon:4565"  
/tissue\_type="endosperm"  
/dev\_stage="developing endosperm tissue 8, 10 and 12 DPA  
(days post anthesis)"  
/clone\_lib="wheat EST endosperm library"

#### ORIGIN

Query Match 25.6%; Score 116.4; DB 5; Length 542;  
Best Local Similarity 94.1%; Pred. No. 1.2e-19;  
Matches 143; Conservative 0; Mismatches 6; Indels 3; Gaps 2;  
QY 195 TGTGATCTGATCCCGCTGTGTGGGAGATGATGCGGCGTTTAAATTT-CGCCATGC 253  
DB 96 TGTGATCTGATCCCGCTGTGTGGGAGATGATGCGGCGTTTAAATTTCCGCATGC 155

QY 254 TAAACAGATCAGAGAGGGAAGGACATGTTATATTTATATTTCTGCG 313  
|||||  
Db 156 TAAACAGATCAGAGAGGGAAGGACATGTTATATTTATATTTCTGCG 215  
|||||  
QY 314 TCGTCTCGTCAGGCTTAGATGTCATGATCT 345  
|||||  
Db 216 TCGTCTCGTCAGGCTTAGATGTCATGATCT 245  
|||||

RESULT 2  
CNS0073W 922 bp DNA linear GSS 03-JUN-1999  
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #  
DEFINITION BACR14D09 of RPCL-98 library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.

ACCESSION AL066784 GI:4945247  
VERSION AL066784.1  
KEYWORDS Drosophila melanogaster (fruit fly)  
SOURCE Drosophila melanogaster  
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 922)  
Genoscope.  
REFERENCE Direct Submission  
AUTHORS Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage;  
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
Determination of this BAC end sequence was carried out as part of a  
collaboration with the Berkeley Drosophila Genome Project (BDGP).  
The BDGP is constructing a physical map of the Drosophila  
melanogaster genome using these BACs. For further information  
please see <http://www.fruitfly.org> The BDGP Drosophila  
melanogaster BAC library was prepared by Kazutoyo Osoegawa and  
Aaron Mamoser in Peter de Jong's laboratory in the Department of  
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
NY. The library is named RPCL-98 and was constructed by partial  
EcoRI digestion of Drosophila DNA provided by the BDGP from the  
isogenic strain y2; cn bw sp, the same strain used for the BDGP's  
p1 and EST libraries. A more detailed description of the library  
and how to order individual BAC clones, the entire library, or  
filters for hybridization from the BACPAC Resource Center can be  
found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES  
source  
1..922  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
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ORIGIN  
Query Match 11.7%; Score 53.2; DB 9; Length 922;  
Best Local Similarity 20.3%; Pred. No. 0.0045;  
Matches 74; Conservative 128; Mismatches 163; Indels 0; Gaps 0;

QY 36 TTTTCTTTCGTCGTCGTCGATCTTTGCGCTTGTGAGTTGGTGGCGAGAGCGC 95  
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Db 542 KTTTCTTTCGTCGTCGTCGATCTTTGCGCTTGTGAGTTGGTGGCGAGAGCGC 601  
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QY 96 TTGCTGGCCAGATCGGTGGCGGAGGCGGAGATCCCGGCTGCGCGCGC 155  
|||||  
Db 602 GTTCTTTCGTCGTCGTCGATCTTTGCGCTTGTGAGTTGGTGGCGAGAGCGC 661  
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QY 156 GAGTCGCGCCGAGATCCGCGGAGAAATGGGCTCTCGAGATGATCTGATCCGCGCTG 215  
|||||  
Db 662 TKTCTTTCGTCGTCGTCGATCTTTGCGCTTGTGAGTTGGTGGCGAGAGCGC 721  
|||||

QY 216 TTGGGAGAGATGAGGCGCTTTAAATTTCCGCGATGCTAAACAGATCAGAGAGGCG 275  
|||||  
Db 722 KKKCTTTCGTCGTCGTCGATCTTTGCGCTTGTGAGTTGGTGGCGAGAGCGC 781  
|||||

QY 276 AAAAGGACATGTTATATTTATATTTCTGCGCTGCTGTCAGGCTTAGATG 335  
|||||  
Db 782 KKK 841  
|||||

QY 336 TCGTAGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 395  
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Db 842 KKK 901  
|||||

QY 396 CGTAG 400  
|::|  
Db 902 GKKKG 906  
|::|

RESULT 3  
AG429940 1083 bp DNA linear GSS 03-JUN-2004  
LOCUS Mus musculus molossinus DNA, clone:MSMg01-304M02.TU, genomic survey  
DEFINITION sequence.  
ACCESSION AG429940 GI:48073003  
VERSION AG429940.1  
KEYWORDS GSS.  
SOURCE Mus musculus molossinus  
ORGANISM Mus musculus molossinus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1  
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.  
TITLE BAC end Sequences of Library MSMg01  
JOURNAL Unpublished  
2 (bases 1 to 1083)  
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.  
REFERENCE Submitted (17-NOV-2003) Maehira Hattori, The Institute of Physical  
JOURNAL and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan  
1-7-22 Suenho-chou, Tsukuba-shi, Ibaraki, Japan 305-0857, Japan  
Tel:81-45-503-9111, Fax:81-45-503-9170  
E-mail:hattori@gsc.riken.jp, URL:<http://hgp.gsc.riken.go.jp/>,  
Tel:81-45-503-9111, Fax:81-45-503-9170  
Clones are derived from the mouse BAC library MSMg01. For BAC  
library availability, please contact Kuniya Abe (abe@tc.riken.jp).  
Tsukuba Institute, Bio Resource Center,  
The Institute of Physical and Chemical Research (RIKEN) 3-1-1  
Koyada, Tsukuba, 305-0074 Japan  
phone: 81-298-36-9189, fax: 81-298-36-9199  
e-mail: abe@tc.riken.jp

PRIMERS  
Sequencing : TU  
LIBRARY  
Vector : pBACe3.6  
R.Site 1 : EcoRI  
R.Site 2 : EcoRI.

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Query Match 11.7%; Score 53.2; DB 9; Length 1083;  
Best Local Similarity 45.4%; Pred. No. 0.0046;  
Matches 187; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

QY 9 CCGGCGCCCTCTCTCTTCTTCTCTCGGTTTCTGTCGCTGATCTTTCGCGC 68  
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Db 234 CGGCTTGTGTTTCTTCTTCTTCTGCGGTTTCTGTCGCTGATCTTTCGCGC 293  
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QY 69 TTGCTAGTTGGGTGGCGAGAGCGGCTTCTGTCGCGCCAGATGCTGCGCGGAGGCGCG 128  
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Db 294 TCGTTTTTTTTTTGGGGGGGGCCGGCGGGGGGGGGGGGGGGGGCCCGGGGGGGCG 353  
 Qy 129 GATCTCGGGGCTGGGCTCTCCGGGGGCTAGTCGCGCCGGATCTCGCGGGGAATGGGGCT 188  
 Db 354 GCGCGGGGGGGGGGGGGGGCGCGGGGGGGGGGGGGGGGGCGGGGGGGGGGGGGGGGG 413  
 Qy 189 CTCGATCTAGATCTGATCCGCGCTGTGTGGGGGAGATGGGGCGTTTAAATTTGGC 248  
 Db 414 GCGGGGGGGCGGGGGGGGGGGCGCGGGGGGGGGGGCGGGTGGGGGGGGGGGGGGGG 473  
 Qy 249 CATGCTAAACAAGATCAGAGAGAGGGGAAAAAGGACATAGTTATATTTTAAATAT 308  
 Db 474 GGGCGTGGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGTTTTTTTTTTTTTTTT 533  
 Qy 309 TCTGCTGCTGCTGTCAGGCTTAGATGTGATCTTCTCTCTCTCTCTCTCTCTCTCTCT 368  
 Db 534 TTGTTTTTTTTTTGTT 593  
 Qy 369 AATTGATCCCTCAGCATGTCTACCGGAGTTTTCTTTTCAGATTTGG 420  
 Db 594 TTCTGTGTGTTTTGTT 645

RESULT 4			
CNS016KT/c			
LOCUS	CNS016KT	1013 bp	DNA linear GSS 26-JUL-1999
DEFINITION	Drosophila melanogaster genome survey sequence SP6 end of BAC		
	BACN16016 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.		

ACCESSION	AL106871
VERSION	AL106871.1
KEYWORDS	GI:5624218
SOURCE	GSS.
ORGANISM	<i>Drosophila melanogaster</i> (fruit fly)
	<i>Drosophila melanogaster</i>
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyndroidea; Drosophilidae; <i>Drosophila</i> .
REFERENCE	1 (bases 1 to 1013)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage

**COMMENT**

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk> . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billard at CBNP (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.

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FEATURES
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            /note="end : SP6"

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	Query Match	Similarity	Score	DB %	length
Best Local	105;	Conservative	105;	Mismatches	222; Indels 3; Gaps 1,
Matches	105;	Conservative	105;	Mismatches	222; Indels 3; Gaps 1,
QY	18	CTCCCTCTTCTTCCTCGTTTTTTTTCGTCGTCGCATCTTTGACCTTTGATGTT	77		
DB	458	CNNCCGKTKKKCN	399		
QY	78	TGGGTGGGCGAGACGGCGCTTCGTCGCCCCAGATCGGTGGCGGAGAGGGCGGAGATTCCGG	137		
DB	358	KNNGCKTKNGKCKCCAGANNKCKKCKCCCKGCKCKKKKKKKKKKKNNKCNNNNNKCNK	339		

Oy	138	GCTGGGCTCCGGGGGTAGTGGCCCGGAAATCTCGGGGAAATGGGGCTCTCGGATGT	197
Db	338	NCCCKMAAANCKKKKDDAAKCKCANMANCAKGTATKCKGKNKAKKSKKKKNKGGKGR	279
Oy	198	AGATCTGATCCGCGCTGTGTGGGGGAGATGATGGGGCTTTAAATTTCCGACATGCTAAA	257
Db	278	NKGGKCKSKGGGGSSRRKGNKNGGSKKAKGKSGKGGKGGKKKKKMAAAGGGKNGGG	219
Oy	258	CAAGATCAGGAAGAGGGGAAAAAGGCACATAGCTTATATTTATATATTTCTGCTGT	317
Db	218	---KKGGGGATATNKKGGKAKACATNNCTNNTKTKCTCTTTBTATTTATCNBTITTT	162
Oy	318	GCTCGTCAAGCTTAGATGTGCTAGATCTTTCTTTCTTTTGTGGGTAGAAATTTGAAT	377
Db	161	TTKTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTNNSTTCNTMNTATNNNTT	102
Oy	378	CCCTCAGCATGTTCATCGGTAGTCTTTCTTTATATGATTTGTACAAATGCAGCCTGT	437
Db	101	CTBTTCABTTTTTNNCNRBTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTNTTGAAT	42
Oy	438	GGGAGCTTTTGT	452
Db	41	TTTAACTTTTNTGT	27

RESULT 5	CNS0071A	LOCUS	DEFINITION
	CNS0071A	895 bp	DNA linear GSS 03-TUN-1995
			Drosophila melanogaster genome survey sequence TET3 end of BAC #
			BACR1B09 of RPL1-99 library from Drosophila melanogaster (fruit
			fly), genomic survey sequence.

ACCESSION	AL066286
VERSION	AL066286.1
KEYWORDS	GI:4945153
SOURCE	GSS.
ORGANISM	Drosophila melanogaster (fruit fly)
	Drosophila melanogaster

REFERENCE	AUTHORS	TITLE	JOURNAL
1 (bases 1 to 895)	Genoscope.	Direct Submission	Submitted (02-JUN-1999) Genoscope - Centre National de Séquençage : BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the *Drosophila melanogaster* genome using these BACs. For further information please see [http://www.fruitfly.org/The\\_BDGP/Drosophila\\_melanogaster\\_BAC\\_library](http://www.fruitfly.org/The_BDGP/Drosophila_melanogaster_BAC_library) was prepared by Kazuhiro Oseegawa and Aaron Mammoeser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCL-98 and was constructed by partial *EcoRI* digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's p1 and Esr1 libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES			
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Best Local Similarity	20.5%	Pred. No. 0.011;	

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RESULT 6  
 LOCUS CDS00600 884 bp DNA linear GSS 03-JUN-1999  
 DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC #  
 BACR14N21 of RPCT-98 library from Drosophila melanogaster (fruit  
 fly), genomic survey sequence.  
 ACCESSION AL065923  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Drosophila melanogaster (fruit fly)  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Ephydroidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 884)  
 Genoscope.  
 REFERENCE  
 AUTHORS  
 TITLE Direct Submission  
 JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
 BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef.genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 COMMENT  
 Determination of this BAC-end sequence was carried out as part of a  
 collaboration with the Berkeley Drosophila Genome Project (BDGP).  
 The BDGP is constructing a physical map of the Drosophila  
 melanogaster genome using these BACs. For further information  
 please see <http://www.fruitfly.org> The BDGP Drosophila  
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and  
 Aatron Mammoser in Pieter de Jong's laboratory in the Department of  
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
 NY. The library is named RPCT-98 and was constructed by partial  
 EcoRI digestion of Drosophila DNA provided by the BDGP from the  
 isogenic strain y2; cn bw sp, the same strain used for the BDGP's  
 P1 and EST libraries. A more detailed description of the library  
 and how to order individual BAC clones, the entire library, or  
 filters for hybridization from the BACPAC Resource Center can be  
 found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).  
 FEATURES  
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RESULT 7			
CNS00655			
LOCUS			
DEFINITION	Drosophila melanogaster genome survey sequence T7 end of BAC # BACR14J09 of RPc1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.	919 bp	DNA linear GSS 03-JUN-1999
ACCESSION	AL065856		
VERSION	AL065856.1	GI:4944824	
KEYWORDS	GSS.		
SOURCE	Drosophila melanogaster (fruit fly)		
ORGANISM	Drosophila melanogaster		
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
AUTHORS	1 (bases 1 to 919)		
TITLE	Genoscope.		
JOURNAL	Direct Submission		
COMMENT	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)		
	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <a href="http://www.fruitfly.org">http://www.fruitfly.org</a> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPc1-98 and was constructed in pBuffal. EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at <a href="http://bacpac.med.buffalo.edu/drosophila_bac.htm">http://bacpac.med.buffalo.edu/drosophila_bac.htm</a> .		
FEATURES	Location/Qualifiers		
Source	1..919		







Oy		5	CCACCCCCCCTTCTTCCTTTCTTCTTCGATTTTTTTCGTGGTGATCATCTT	64
Dd		982	BSCSCSGSSCGSSTYTTTTTTTTCCKSSBTTTKCMKGCKSTSNNGGCCSCTY	923
Oy		65	GGCCTTGATATTGGGTGGAGCAAGCGGCTTCGTCCGCCAATCGATGGCGCAGAGG	124
Dd		922	YGCTYTSCGYTTBSGCCSSCSGSCTXKSTRTCCGSSCSSGASACSBTSNTSCSTWS	863
Oy		125	CGCGGATTCGCCGCTGCGCTTCGCCGCGGTGAATCGGCCCGGATCTCTCGGGAAATCG	184
Dd		862	GCKSSFGCGSCSGSSGGCTTCGSHBGCKCGGSCSBSSTFCGSGSGCCSCTSTCYTWS	803
Oy		185	GGCTTCGGATGTAGATCTGATCCGCGCCCTTGAGGAGGAGATGAT	229
Dd		802	TGSSSGSSSTKTCGSKCSCGSGGSGSTGSBSCGSGCGGCERT	758
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RESULT 12				
CL496209/c				
LOCUS		CL496209	1656 bp	DNA linear GSS 01-APR-2004
DEFINITION		SAIL_620_H08.v1 SAIL Collection Arabidopsis thaliana genomic clone		
ACCESSION		CL496209		
VERSION		GI:45988295		
KEYWORDS		GSS.		
SOURCE		Arabidopsis thaliana (thale cress)		
ORGANISM		Arabidopsis thaliana		
REFERENCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroside II; Brassicales; Brassicaceae; Arabidopsie.		
AUTHORS		I (bases 1 to 1656) Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D., Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cocton,D., Bullis,D., Shell,J., Miguel,T., Hutchison,D., Kimmerly,B., Mitzel,T., Katagiri,F., Glazebrook J., Law,M. and Gottf,S.A. A high-throughput Arabidopsis reverse genetics system Plant Cell 14 (12), 2985-2994 (2002)		
JOURNAL MEDLINE PUBMED		12468722		
COMMENT		Contact: Sessions A Applied Trait Genetics Syngenta Biotechnology Inc. 3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA Email: allen.sessions@syngenta.com ABRC Stock Number CS826580; T-DNA left border flanking sequences of Syngenta Arabidopsis Insertion Library (SAIL) lines are available through the Arabidopsis Biological Resource Center (ABRC). Sequences represent a pool of amplified genomic regions and not single contiguous sequences. Class: TDNA tagged.		
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Best Local Similarity		51.2%; Pred. No. 0.14;	99;	Indels 0;
Matches		104;	Conservative 0;	Mismatches 99;
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Oy		65	GACCTTGTAGTTGGGTGGAGCAAGCGGCTTCGTCCGCCAATCGATGGCGCAGAGG	124
Dd		391	CCTCTTTTGTGGGGGTGGAGGTGTGTGTGCGCGCGCTGTGANCSCGGGGGGGG	332

[illegible]

Db		492	TTNTTTTKTTTTWACAAAAAATAAAAAAAAAATTAATTAAATAAATTAATTAATTT	551
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Db		552	WTTTTTTTTTTTTTTCTAAATTTTWTAAATTAATTAATTTTTTTTTTAATTTATTTWKTG	611
Oy		364	GATGAATTTGAATCCCTCAGCATGTGCATCGGAGATTTTCTTTTCATGATTTGT	420
Db		612	TTTWATTTTATTTTWTATTTTATTTTTTTTTTTWWTTTTTTTTTTTATTAATMAT	668
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RESULT 14				
LOCUS	CNS0175/c			
DEFINITION	CNS0175Y	1101 bp	DNA	linear GSS 26-JUL-1999
ACCESSION	Drosophila melanogaster genome survey sequence Sp6 end of BAC			
VERSION	BACN37L08 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.			
KEYWORDS	AL108460			
SOURCE	ALI08460.1 GI:5628764			
ORGANISM	GSS.			
REFERENCE	Drosophila melanogaster (fruit fly)			
AUTHORS	Drosophila melanogaster			
TITLE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.			
JOURNAL	1 (bases 1 to 1101)			
COMMENT	Genoscope. Direct Submission Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr) Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CBPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Buchton and Genevieve Payan. It has been constructed in the vector pBelobAC11.			
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	Matches	33;	Conservative 119;	Mismatches 72; Indels 0; Gaps 0;
Oy	1	GTAACCACCCGCCCTCTCCTCTTCTTCTCCGTTTCTTTTCTTCGCTCGATCGAT	60	
Db	1033	STSSSSSSSTSSSSSTSBHBTSTSSSSSTTTTCTTTTSTTBBSBSBSSSTS	974	
Oy	61	CTTGGCCCTGGTAGTTGGGAGCGAGAAGCGGCTTGTCGACAGATCGGCGGAG	120	
Db	973	SSBRTSKBPTBSBSSTSSASABSSSSSSBSBSTTBSBBSBTSSSSSBSBS	914	
Oy	121	AGGGCGGAGATCTCGCGCTGCGCTCCCGCGCGTGAATCGAGCCCGATCTCGCGGGA	180	
Db	913	TBSBSBHBTBTBTSTSSSTSBHTTTBSBSSSSSSBSBSTTBSBSSTBSY	854	
Oy	181	ATGGGCTCTCGATGTAGATGTATCCGCCCTTTGTTGGGAG	224	
Db	853	GSSBRTCKSCSTBTSGBTBSBMSKBSSTSTBTSGBCSBCG	810	

LOCUS	CV3131848	602 bp	mRNA	linear	EST 03-SEP-2004
DEFINITION	L3P09g04 Populus stem seasonal library Populus deltoides cDNA, mRNA sequence.				
ACCESSION	CV3131848				
VERSION	CV3131848.1	GI:51875768			
KEYWORDS	EST.				
SOURCE	Populus deltoides				
ORGANISM	Populus deltoides				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.				
AUTHORS	1 (bases 1 to 602) Park S. and Han, K.-H.				
TITLE	Gene expression profile during seasonal growth cycle in poplar tree				
JOURNAL	Unpublished (2003)				
COMMENT	Contact: Kyung-Hwan Han Department of Forestry Michigan State University 126 Natural Resources, East Lansing, MI 48824-1222, USA Tel: 517 353 4751 Fax: 517 432 1143 Email: hanky@msu.edu.				
FEATURES	Location/Qualifiers				
source	1..602 /organism="Populus deltoides" /mol_type="mRNA" /strain="IL-129" /db_xref="taxon:3696" /tissue_type="stem" /dev_stage="1 year old" /clone_id="Populus stem seasonal library"				
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Best Local Similarity	47.9%;	Pred. No. 0.43;			
Matches 162;	Conservative 0;	Mismatches 174;	Indels 2;	Gaps 1;	
QY	40 TTTTTCGTCGCGTCGATCTTTGGCCCTTGTAATTGSGTGAGAGCGGCTTCG	99			
DB	368 TTTTCCTCTGGGGGGGGAATGTTGGAGGGGGGCTTTTGGCTTT	309			
QY	100 TCGCCCAAGATCGTGCCGGAGGGGCGGAGATCTCGCGCTTCGCCGCGTAGT	159			
DB	308 TCCCCCCCCGGGGGAGAGGGGGGGGGGGCCAGGGGCTTTAGGGGGGGAACGGCCGGGCT	249			
QY	160 CGGCGCGGAGTCCTGCGGGGGAATGGGGGCTCGGAGTAGATCGATCCGCCGTTGTGG	219			
DB	248 TTTTCCCGCCCGGGGGGGAACGGGGGGCGCGGAGTAGTAT-TGGGCCCCCTTGG	191			
QY	220 GGGAGATGATGGGCGCTTAAATTTTGGCATGCTAAACAAGATCAGAGAGGGGAAAA	279			
DB	190 GGGGGAGTGGGGGCTCCCGCGGGGGGGGGCGCTTTTGGAAAGTTTGGGGGGGGGGGG	131			
QY	280 GGGCACTAGTGTATATTTTATATATTTCTGCTGCTCGTCAGGCTTAAATGTGCT	339			
DB	130 GGGGGGCGAGGTT	71			
QY	340 AGATCTTCTTCTTCTTTTGTGGGAGAAATTGAT	377			
DB	70 TTTTTTTTTTTTTTTTTTTTTTTTTTTAAATATATATAT	33			

Search completed: September 12, 2005, 03:55:35

Job time : 1196.88 secs







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1 NAME: TIMIN, SUSAN J.
2 REGISTRATION NUMBER: 34,103
3 REFERENCE/DOCKET NUMBER: 19603/10140
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: 716-263-1636
6 TELEFAX: 716-263-1600
7 INFORMATION FOR SEQ ID NO: 7:
8 SEQUENCE CHARACTERISTICS:
9 LENGTH: 1404 base pairs
10 TYPE: nucleic acid
11 STRANDEDNESS: single
12 TOPOLOGY: linear
13 MOLECULE TYPE: CDNA
14 US-08-144-602B-7

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Best Local Similarity	93.5%	Pred. No. 2.3e-105		
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OY	6	CACCCGCGCCCTCTCTCTTTCTTCTCCGATTTTTTTTTTTCGATCGGATCTGATCTTGG	65
Db	936	CCCCGCGCTCCTCTCTCTTTCTTCTCCGATTTTTTTTTTTCGATCGGATCTGATCTTGG	995
OY	66	GCTTTGTAGTTTGGGTGGCGAGACGGCTTCGTCCCGCCAGATCGGTGCGCGGAGGGG	125
Db	996	GCTTTGTAGTTTGGGGGGCGGAGAG-CGGGCTTCGTCCCGCCAGATCGGTGCGCGGAGGGG	1054
OY	126	CGGAGATCTCGGGGCGTGGGGGTCTCCGGGGGGTGAATGCGCGCGGATCTCGCGGGGAATGGG	185
Db	1055	CGGAGATCTCGGGGCTGG-----GTCTCGGGGTGGCGCGGATCTCGCGGGGAATGGG	1107
OY	186	GCTCTCGGATGTAGATCTGATCCGCGTGTGTGGGGAGATGATGGGGCTTTAAATTT	245
Db	1108	GCTCTCGGATGTAGATCTGATCCGCGTGTGTGGGGAGATGATGGGGCTTTAAATTT	1167
OY	246	CGCCATGCTAAACAAGATCAGAAAGAAGGGAAAGAAGCACTAATGTTATATATTTATAT	305
Db	1168	CGCCATGCTAAACAAGATCAGAAAGAAGGGAAAGAAGCACTAATGTTATATATTTATAT	1227
OY	306	ATTTCGTGCTGCTGCTCAGGCTTAGATGTCCTAGATCTTCTCTCTTTTGTGGG	365
Db	1228	ATTTCGTGCTGCTGCTCAGGCTTAGATGTCCTAGATCTTCTCTCTTTTGTGGG	1287
OY	366	TAGAATTTGAATCCCTCAGCATGTTTCATCGGTAGTTTTCTTTTCATGATTTGTGACA	425
Db	1288	TAGAATTTGAATCCCTCAGCATGTTTCATCGGTAGTTTTCTTTTCATGATTTGTGACA	1344
OY	426	ATGCAGCCTCGTGGGAGCTTTTGTGAG	454
Db	1348	ATGCAGCCTCGTGGGAGCTTTTGTGAG	1376

RESULT 6  
 US-08-144-602B-5  
 Sequence 5, Application US/08144602B  
 Patent No. 5641876  
 GENERAL INFORMATION:  
 APPLICANT: MCELROY, David  
 APPLICANT: WU, Ray  
 TITLE OF INVENTION: RICE ACTIN GENE AND PROMOTER  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP  
 STREET: CLINTON SQUARE, P.O. BOX 1051  
 CITY: ROCHESTER  
 STATE: NEW YORK  
 COUNTRY: USA  
 ZIP: 14603  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

```

1      CURRENT APPLICATION DATA:
2      APPLICATION NUMBER: US/08/144,602B
3      FILING DATE: 27-OCT-1993
4      CLASSIFICATION: 536
5      ATTORNEY/AGENT INFORMATION:
6      NAME: TIMIAN, SUSAN J.
7      REGISTRATION NUMBER: 34,103
8      REFERENCE/DOCKET NUMBER: 19603/10140
9      TELECOMMUNICATION INFORMATION:
10     TELEPHONE: 716-263-1636
11     TELEFAX: 716-263-1600
12     INFORMATION FOR SEQ ID NO: 5:
13     SEQUENCE CHARACTERISTICS:
14     LENGTH: 2199 base pairs
15     TYPE: nucleic acid
16     STRANDEDNESS: single
17     TOPOLOGY: linear
18     MOLECULE TYPE: CDNA
19
20     US-08-144-602B-5

```

Query Match	83.6%;	Score	379.4;	DB	1;	Length	2199;
Best Local Similarity	93.5%;	Pred. No.	3e-105;				
Matches	420;	Conservative	0;	Mismatches	21;	Indels	8;
						Gaps	2

[illegible]

```

RESULT 7
; US-08-144-602B-4
; Sequence 4, Application US/08144602B
; Patent No. 5641876
; GENERAL INFORMATION:
; APPLICANT: McILROY, David
; APPLICANT: WU, Ray
; TITLE OF INVENTION: RICE ACTIN GENE AND PROMOTER
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
; STREET: CLINTON SQUARE, P.O. BOX 1051
; CITY: ROCHESTER
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 14603
;

```



```

COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/144,602B
FILING DATE: 27-OCT-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: TIMIAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/10140
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 5643 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-144-602B-4

Query Match      83.6%; Score 379.4; DB 1; Length 5643;
Best Local Similarity 93.5%; Pred. No. 5e-105;
Matches 420; Conservative 0; Mismatches 21; Indels 8; Gaps 2;

QY      6 CACCCGCCCCCTCCTCTTTCTTTCTTCGTTTTTTTGCTCGCTCGATCTTTG 65
DB      1736 CCCGGCCTCCCTCCTCTTTCTTTCTTCGTTTTTTTGCTCGCTCGATCTTTG 1795

QY      66 GCCTTGTAATTGGGTGGCGAGAGCGGCTTCGTGCCAGATCGGTGCGGGAGGG 125
DB      1796 GCCTTGTAATTGGGTGGCGAGAG-CGGCTTCGTGCCAGATCGGTGCGGGAGGG 1854

QY      126 CGGAGATTCGGCGGTGGCGTCTCCGGGCGTAGTCCGACCAGATCTCGCGGGAAATGG 185
DB      1855 CGGAGATTCGGCGGTGG-----GTCGCGCGTGGCGGCGGATCTCCGCGGGAAATGG 1907

QY      186 GCTCTCGGATGTGAATGCAGCCGCTGTGGGGGAGAATATGAGGGGCTTTAAAATT 245
DB      1908 GCTCTCGGATGTGAATGCAGCCGCTGTGGGGGAGAATATGAGGGGCTTTAAAATT 1967

QY      246 CGCATCTATAAAGATCAGAAAGAGGGGAAAGGCACTAGTATTATTTTAAAT 305
DB      1968 CGCATCTATAAAGATCAGAAAGAGGGGAAAGGCACTAGTATTATTTTAAAT 2027

QY      306 ATTTCTGCTGCTCTGCTCAGGCTTAGATGCTAGATCTTTCTTTCTTTTGTGG 365
DB      2028 ATTTCTGCTGCTCTGCTCAGGCTTAGATGCTAGATCTTTCTTTCTTTTGTGG 2087

QY      366 TAGAATTGATCCCTCAGATTTGTTTCATCGTAGTTTCTTTTATGATTGGACA 425
DB      2088 TAGAATTGATCCCTCAGATTTGTTTCATCGTAGTTTCTTTTATGATTGGACA 2147

QY      426 ATGAGCGCTGCTGCGAGGCTTTTGTGAG 454
DB      2148 ATGAGCGCTGCTGCGAGGCTTTTGTGAG 2176

RESULT 8
US-09-377-466B-19
Sequence 19, Application US/09377466B
Patent No. 6501009
GENERAL INFORMATION:
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Expression of Cry3Ab Insecticidal Protein in Plants
FILE REFERENCE: 38-21(15304) Cry3Ab Improved Exp. Corn
CURRENT APPLICATION NUMBER: US/09/377,466B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43

```

```

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 3039
; TYPE: DNA
; ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: expression
OTHER INFORMATION: cassette
NAME/KEY: promoter
LOCATION: (14)..(235)
OTHER INFORMATION: P-CamV.AS4
NAME/KEY: 5'UTR
LOCATION: (240)..(304)
OTHER INFORMATION: L-Ta.hcb1
NAME/KEY: Intron
LOCATION: (318)..(805)
OTHER INFORMATION: I-Os.Act1
NAME/KEY: CDS
LOCATION: (811)..(2769)
OTHER INFORMATION: Cry3Bb1 variant 11231mw1
NAME/KEY: Terminator
LOCATION: (2787)..(3020)
OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-19

Query Match          78.4%; Score 355.8; DB 4; Length 3039;
Best Local Similarity 92.9%; Pred. No. 5.6e-98;
Matches 430; Conservative 0; Mismatches 22; Indels 11; Gaps 5;

QY      1 GTTACCACCCCGCCCTCCTCTTTCTTCCTGTTTTTTTTTGATCGGTCTCGAT 60
DB      334 GTAACCAACCCCGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCAT 393
QY      61 CTCTGGCTTGTGATGTTGGAGGAGGAGA---GCAGCTTCGCCAATCGATGCG 116
DB      394 CTCTGGCTTGTGATGTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 453
QY      117 CGGAGGGGCGGAGATCTCGCGGCTGGCGTCTCG--GGCTGATGCGCCCGGATCTCG 174
DB      454 CGGAGGGGCGGAGATCTCGCGGCTGGGCTCTCGCGGCTGATGATCGGATCTCG 513
QY      175 CGGGAATGGGCGCTCGGATGATGATCT--GATCGCGCGTGTGGGGAGATGATGGG 232
DB      514 CGGGAATGGGCGCTCTCGGATGATGATGATCGGATCGCGGATGATGATGATG 573
QY      233 GCCTTTAAATT--CGCATGCTTAACAAGATCAGAGAGGAGAAAAGGCACTATGAT 291
DB      574 GGCTTTAAATTTCGCCCGGCTTAACAAGATCAGAGAGGAGAAAAGGCACTATGAT 633
QY      292 TTATATTTTATATATTTCTGCTGCTGCTGCTGCTGATGATGATGATGATGATGAT 351
DB      634 TTATATTTTATATATTTCTGCTGCT--TCGACAGGCTTAGATGATGATGATGAT 691
QY      352 CTCTCTTTTGTGGGTGAATTTGAATCCCTGACAGATGTTCAATCGATGATTTCTTTTC 411
DB      692 CTCTCTTTTGTGGGTGAATTTGAATCCCTGACAGATGTTCAATCGATGATTTCTTTTC 751
QY      412 ATGATTTTGACAAATGACAGCCTCGGCGGAGACTTTTGTGTAG 454
DB      752 ATGATTTTGACAAATGACAGCCTCGGCGGAGACTTTTGTGTAG 794

RESULT 9
US-09-377-466B-21
; Sequence 21, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43

```

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/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 21
/ LENGTH: 3039
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: expression
/ OTHER INFORMATION: cassette
/ NAME/KEY: promoter
/ LOCATION: (14)..(235)
/ OTHER INFORMATION: P-CAMV.AS4
/ NAME/KEY: 5' UTR
/ LOCATION: (240)..(304)
/ OTHER INFORMATION: L-Ta.hcb1
/ NAME/KEY: Intron
/ LOCATION: (318)..(805)
/ OTHER INFORMATION: I-08.Act1
/ NAME/KEY: CDS
/ LOCATION: (811)..(2769)
/ OTHER INFORMATION: Cry3Bb1 variant 11231mv2
/ NAME/KEY: terminator
/ LOCATION: (2787)..(3020)
/ OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-21
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Query Match          78.4%; Score 355.8; DB 4; Length 3039;
Best Local Similarity 92.9%; Pred. No. 5.6e-98;
Matches 430; Conservative 0; Mismatches 22; Indels 11; Gaps 5;
```

```
QY      1 GTAACCAACCCGCCCTCTCTCTTTCTTCGCTTTTTCGTCGTCGATCGAT 60
DB      334 GTAACCAACCCGCCCTCTCTCTTTCTTCGCTTTTTCGTCGTCGATCGAT 393
QY      61 CTTTGCCCTTGTAAGTTTGGTGGGCGAGA----GCGCTTCGTCGCCGATCGATCG 116
DB      394 CTTTGCCCTTGTAAGTTTGGTGGGCGAGAAGCGCGCTTCGCGCCGATCGATCG 453
QY      117 CCGGAGGGGGCGGAGATCTCGGCGCTGGCGCTCCG--GGCGTGAATCGGCCCGATCCTCG 174
DB      454 CCGGAGGGGGCGGAGATCTCGGCGCTGGCGCTCCGCGCTCGATCGGCCCGATCCTCG 513
QY      175 CCGGGAATGGGAGCTCTCGATGTAGATCT--GATCCGCCCTTGTGGGGGAGATGATGG 232
DB      514 CCGGGAATGGGAGCTCTCGATGTAGATCTCGATCGATCCGCCCTTGTGGGGGAGATGATGG 573
QY      233 GCGTTTAAATTT--CGCATGCTTAAACAAGATCAGGAAGAGGGAAGGCACTATGCT 291
DB      574 GGGTTTAAATTTCCGCCGTAAACAAGATCAGGAAGAGGGAAGGCACTATGCT 633
QY      292 TTATATTTTATATATTTCTGCTGCTGCTCGTCAAGCTTAGATGCTAGATCTTTCTTT 351
DB      634 TTATATTTTATATATTTCTGCTGCT--TCGTCAAGCTTAGATGCTAGATCTTTCTTT 691
QY      352 CTTCTTTTGTGGTAGAATTTGAATCCCTCAGCATTTTCATCGTAGTCTTTCTTTTC 411
DB      692 CTTCTTTTGTGGTAGAATTTGAATCCCTCAGCATTTTCATCGTAGTCTTTCTTTTC 751
QY      412 ATGATTTGTGACAAATGCAAGCTCGTCGAGAGCTTTTGTAG 454
DB      752 ATGATTTGTGACAAATGCAAGCTCGTCGAGAGCTTTTGTAG 794
```

```
RESULT 10
US-09-377-466B-38
/ Sequence 38, Application US/09377466B
/ Patent No. 6501009
/ GENERAL INFORMATION:
/ APPLICANT: Romano, Charles P.
/ TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
/ FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
/ CURRENT APPLICATION NUMBER: US/09/377,466B
/ CURRENT FILING DATE: 1999-08-19
/ NUMBER OF SEQ ID NOS: 43
```

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/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 38
/ LENGTH: 3044
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: expression
/ OTHER INFORMATION: cassette
/ NAME/KEY: promoter
/ LOCATION: (14)..(235)
/ OTHER INFORMATION: P-CAMV.AS4
/ NAME/KEY: 5' UTR
/ LOCATION: (240)..(304)
/ OTHER INFORMATION: L-Ta.hcb1
/ NAME/KEY: Intron
/ LOCATION: (318)..(805)
/ OTHER INFORMATION: I-08.Act1
/ NAME/KEY: CDS
/ LOCATION: (811)..(2769)
/ OTHER INFORMATION: variant Cry3Bb1 coding sequence encoding v11231
/ NAME/KEY: terminator
/ LOCATION: (2782)..(3025)
/ OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-38
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Query Match          78.4%; Score 355.8; DB 4; Length 3044;
Best Local Similarity 92.9%; Pred. No. 5.6e-98;
Matches 430; Conservative 0; Mismatches 22; Indels 11; Gaps 5;
```

```
QY      1 GTAACCAACCCGCCCTCTCTCTTTCTTCGCTTTTTCGTCGTCGATCGAT 60
DB      334 GTAACCAACCCGCCCTCTCTCTTTCTTCGCTTTTTCGTCGTCGATCGAT 393
QY      61 CTTTGCCCTTGTAAGTTTGGTGGGCGAGA----GCGCTTCGTCGCCGATCGATCG 116
DB      394 CTTTGCCCTTGTAAGTTTGGTGGGCGAGAAGCGCGCTTCGCGCCGATCGATCG 453
QY      117 CCGGAGGGGGCGGAGATCTCGGCGCTGGCGCTCCG--GGCGTGAATCGGCCCGATCCTCG 174
DB      454 CCGGAGGGGGCGGAGATCTCGGCGCTGGCGCTCCGCGCTCGATCGGCCCGATCCTCG 513
QY      175 CCGGGAATGGGAGCTCTCGATGTAGATCT--GATCCGCCCTTGTGGGGGAGATGATGG 232
DB      514 CCGGGAATGGGAGCTCTCGATGTAGATCTGATCGATCCGCCCTTGTGGGGGAGATGATGG 573
QY      233 GCGTTTAAATTT--CGCATGCTTAAACAAGATCAGGAAGAGGGAAGGCACTATGCT 291
DB      574 GGGTTTAAATTTCCGCCGTAAACAAGATCAGGAAGAGGGAAGGCACTATGCT 633
QY      292 TTATATTTTATATATTTCTGCTGCTGCTCGTCAAGCTTAGATGCTAGATCTTTCTTT 351
DB      634 TTATATTTTATATATTTCTGCTGCT--TCGTCAAGCTTAGATGCTAGATCTTTCTTT 691
QY      352 CTTCTTTTGTGGTAGAATTTGAATCCCTCAGCATTTTCATCGTAGTCTTTCTTTTC 411
DB      692 CTTCTTTTGTGGTAGAATTTGAATCCCTCAGCATTTTCATCGTAGTCTTTCTTTTC 751
QY      412 ATGATTTGTGACAAATGCAAGCTCGTCGAGAGCTTTTGTAG 454
DB      752 ATGATTTGTGACAAATGCAAGCTCGTCGAGAGCTTTTGTAG 794
```

```
RESULT 11
US-09-377-466B-17
/ Sequence 17, Application US/09377466B
/ Patent No. 6501009
/ GENERAL INFORMATION:
/ APPLICANT: Romano, Charles P.
/ TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
/ FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
/ CURRENT APPLICATION NUMBER: US/09/377,466B
/ CURRENT FILING DATE: 1999-08-19
/ NUMBER OF SEQ ID NOS: 43
```

```

1 SOFTWARE: PatentIn Ver. 2.0
2 SEQ ID NO 17
3 LENGTH: 3450
4 TYPE: DNA
5 ORGANISM: Artificial Sequence
6 FEATURE:
7 OTHER INFORMATION: Description of Artificial Sequence: expression
8 NAME/KEY: promoter
9 LOCATION: (14)..(235)
10 OTHER INFORMATION: P-CaMV.AS4
11 NAME/KEY: 5' UTR
12 LOCATION: (240)..(304)
13 OTHER INFORMATION: L-Ta.hcb1
14 NAME/KEY: intron
15 LOCATION: (318)..(805)
16 OTHER INFORMATION: I-Or.Act1
17 NAME/KEY: transit_peptide
18 LOCATION: (825)..(971)
19 OTHER INFORMATION: amino terminal TS-Zm.rpcs
20 NAME/KEY: intron
21 LOCATION: (972)..(1134)
22 OTHER INFORMATION: I-Zm.rpcs
23 NAME/KEY: transit_peptide
24 LOCATION: (1135)..(1221)
25 OTHER INFORMATION: carboxy terminus TS-Zm.rpcs
26 NAME/KEY: CDS
27 LOCATION: (1222)..(3180)
28 OTHER INFORMATION: Cry3Bb1 variant 11231mw1
29 NAME/KEY: terminator
30 LOCATION: (3198)..(3431)
31 OTHER INFORMATION: T-Ta.hep17
32 JS-09-377-4668-17

```

Query Match	78.4%	Score 355.8	DB 4	Length 3450
Best Local Similarity	92.9%	Pred. NO. 6e-98		
Matches 430, Conservative	0	Mismatches 22	Indels 11	Gaps 5

**QY**

I GTTACCAACCCCGCCCCCTCTCCTCTTCCTTCCTCCGTTTTTTTTCGGCTCGCTCGAT 60

61 CTTTGGCCCTTGGTACCTTTGGCGTGGCGAGA---GGCGCTTCGTGCGCCAGATCGGTGCG 11

Db 394 CTTTGCCCTTGCTAGTTGGGTGGCGAGAGCGGCTTCGTGCGCCGACAGATCGTCC 45

117 CCGGAGGGCGGGANTCTGCGCGGCTGCGGCTCTCCG---GGCCGTCAGATCCGCCCCGATCTCG I

175 CCGGGAATGGGGCTCTCGGATGATGATCT--GATCGCCCTTCTTGGGGGAGATGATGGG 23

Db 514 CGGGGAATGCGGCTCTCGGATGAGATCTGCATCCGCCCTGTGTTGGGGGAGATGATGGG 57

Db 574 GGGTTTAAATTTCCGCGGTGTTAAACAGATCAGGAAGAGGGGAAAAAGGGCACTATGCT 63

292 TTATATTTTATATATTTCTGCTGCTGCTCAGGCTAGATGTGCTAGATCTTTCTTT 35

634 TATATTTTATATATTCIGCT--TCGTACGCTTAGANGNGTAGATCTTCTT 69

692 CTTCTTTTCTGGTAGATTGATCCCTCAGCATTTGTCATCGGTGTTTTCTTTTC 75

412 ATGATTTTGCAACAATGCAGCCTCGTGCGAGCTTTTGTG 454

US-09-377-466B-36

```

; Sequence 36, Application US/0937746B
; Patent No. 6501009
;
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cyt3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cyt3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 36
;

```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
OTHER INFORMATION: Description of Artificial Sequence: expression
OTHER INFORMATION: cassette
```

LOCATION: (14)..(235)  
OTHER INFORMATION: P.CaM.V.AS4

INSTRUMENT: 301R  
LOCATION: (240) . (304)  
OTHER INFORMATION: T-7a hch1

NAME/KEY: intfon  
LOCATION: (318)..(805)

```

; NAME/KEY: transit_peptide
; LOCATION: (825)..(971)

```

OTHER INFORMATION: of Zea mays rbcS intron  
NAME/KEY: intron

```

LOCATION: 0121: (1121)
;
OTHER INFORMATION: I-Zm.rbcS
NAME/KEY: transit peptide

```

OTHER INFORMATION: TS-2m, rbcS carboxy terminus coding sequence  
 OTHER INFORMATION: downstream of 70s mays rbcS intron

```
NAME/KEY: CDS
LOCATION: (1222) . (3180)
```

```

; NAME/KEY: terminator
; LOCATION: (3198)..(3431)

```

US-09-377-466B-36

Query match	10.4%	score 333.0, $2d \pm 1$	length 3330
Best Local Similarity	92.9%	Pred. No. 6e-98;	Indels 11; Gaps 5;
Matches 420; Conservative	0;	Mismatches 22;	

27 1 GTAAACACCCGCGCCCTCTCCTCTTCTTTCTCCGTTTCTTTTCTTTCGTCCTCGGCTCCGAT 60

Db 334 GTACACACCCGCCCTCTCTCTTTCTTCTCCGTTTTTTCCGTCGGGTCCAT 393

Db 394 CTTTCGACCTTGTAAGTTTGGGTGGGAGAGAGCGCTTTCGTGCGCGCCAGATCGTTCG 453

117 CGGAGGGGCGGATCTCGGGCTGGCGTCCG--GGCGTAGTCGGCCCGGATCCTCG 174

176 CCCCCCAGGCGGGGACCTTCCATTTTCCTTGTGGGAGATGCATTGGG 212

514 CGGGGATGGGGCTCTCGAATGTAGATCTCGATCCGCCGTTGTTGGGGGAGATGATGGG 573

233 GCGTTAAATTT-CGCGATGCTAAACAAGATCAGCAGAGAGGGGAAAAGGGCACTATGCT 291

292 TTATATTTTATATATTTCTGCTGCTGCTCGTCAAGCTTAGATGTGCTAGATCTTTCTTT 351

Db 634 TTATATTTTATATATTTCTGCTGT--TCTCAGGCTAGATGCTAGATCTTTCTTT 691

Qy	352	TTTCTTTTGGGGTAATTTGAATCCCGACACTGGTAAACGGTATTTTCCTTC	411
Db	692	CTTCTTTTGGGGTAATTTGAATCCCGACACTGGTAAACGGTATTTTCCTTC	751
Qy	412	ATGATTTTGACAATSCAGCCTCGTGGGAGCTTTTTTGTAG	454
Db	752	ATGATTTTGACAATSCAGCCTCGTGGGAGCTTTTTTGTAG	794

## RESULT 13

```

US-09-377-466B-23
; Sequence 23, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15104) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 3469
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; NAME/KEY: promoter
; LOCATION: (25)..(640)
; OTHER INFORMATION: P-CaMV.35S
; NAME/KEY: 5'UTR
; LOCATION: (664)..(734)
; OTHER INFORMATION: L-Ta.hcb1
; NAME/KEY: intron
; LOCATION: (748)..(1238)
; OTHER INFORMATION: I-O8.Accl1
; NAME/KEY: CDS
; LOCATION: (1241)..(3199)
; OTHER INFORMATION: Cry3Bb1 variant 1123imv2
; NAME/KEY: terminator
; LOCATION: (3217)..(3450)
; OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-23

```

Query Match	78.4%;	Score 355.8;	DB 4,	Length 3469;
Best Local Similarity	92.9%;	Pred. No. 6e-98;		
Matches 430; Conservative	0;	Mismatches 22;	Indels 11;	Gaps 5;

[illegible]

Oy	352	CTTCCTTTTGGGGAGAAATTGATACCTCAGACATTCTTATCGAGTCTTTCTTTC	411
Db	1122	CTTCCTTTTGGGGAGAAATTGAAATCCCTAGACATTCTTATCGAGTCTTTCTTTC	1189
Oy	412	ATGATTTTGACAAATGAGCCTCTGTGGGAGCTTTTGTGAG	454
Db	1182	ATGATTTTGACAAATGAGCCTCTGTGGGAGCTTTTGTGAG	1224

## RESULT 14

```

US-09-068-101-5
/ Sequence 5, Application US/09068101
/ Patent No. 6372960
/
/ GENERAL INFORMATION:
/ APPLICANT: PLANT GENETIC SYSTEMS N.V.
/ TITLE OF INVENTION: Improved Barstar Gene
/ FILE REFERENCE: 2121-139P
/ CURRENT APPLICATION NUMBER: US/09/068,101
/ CURRENT FILING DATE: 1998-08-26
/ EARLIER APPLICATION NUMBER: EP 96202446.9
/ EARLIER FILING DATE: 1996-09-03
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 5
/
/ LENGTH: 4032
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: other nucleic
/ OTHER INFORMATION: acid, "plasmid pmv71"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1995)..(3400)
/ OTHER INFORMATION: label = PRAC1, "promoter region of rice actin gene"
/ OTHER INFORMATION: - contains an intron in the leader"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (3401)..(3676)
/ OTHER INFORMATION: label = barstar, "barstar DNA"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (3677)..(4003)
/ OTHER INFORMATION: label = 3'nos, "region containing 3' untranslated
/ OTHER INFORMATION: end of nopaline synthase gene of Agrobacterium"
/ OTHER INFORMATION: 1-DNA"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (3399)..(3404)
/ OTHER INFORMATION: label = NcoI, "NcoI recognition site"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (4016)..(4021)
/ OTHER INFORMATION: label = KpnI, "KpnI recognition site"
/
US-09-068-101-5

```

Query Match	76.7%;	Score	348;	DB	3;	Length	4032;
Best Local Similarity	93.1%;	Pred. No.	1.6e-95;				
Matches	432;	Conservative	0;	Mismatches	20;	Indels	12;
						Gaps	6

QY	1	GTAAACACCCCGCCCTCTCCCTCTTCTCTTCCGCTTTTTTTTT--CGCTCCGAGCTCGA	59
Db	2932	GTAAACACCCCGCCCTCTCCCTCTTCTCTTCTCCGCTTTTTTTTTCCGCTCCGAGCTCGA	299
QY	60	TCCTTGCGCTTGGTAGTTCGGGTGGCGCAGA---GCGGCTTCGTCCGCCAGATCGGTCC	115
Db	2992	TCCTTGCGCTTGGTAGTTCGGGTGGCGCAGAGCGGCTTCGTCCGCCGCCAGATCGGTCC	305
QY	116	GCGGGAGGGGGGGGATCTCGCGCGCTGGCGGTCTCGS--GGCGGAGTCGGGCCCGGATCCCTC	173
Db	3052	GCGGGAGGGGGGGGAGTCTCGCGCGCTGGGAGCTCTCGCCGGCGTGAATCCGAGCCCGGATCTC	311
QY	174	GCGGGGAATGGGAGCTCTCGAGTGTAGATCT--GATCGCCGCTGTGTGGGGGAGATGATCG	231

Db	3112	GGGGGGAATGGGGGCTCTGGAGTGTGATCTGGATCCGCGCTTTGTGGGGAGATGATGG	3171
Qy	232	GGCGTTTAAATTT--CGCATGCTTAAACAATCATGAAAGGGGAAAAGGGCACTATGG	290
Db	3172	GGGGTTTAAATTTCCGCGCATGTAAACAAGTCTGGAAAGGGGAAAAGGGCACTATGG	3231
Qy	291	TTTATATTTTATATATTTCTGCTGCTCTGTCAGGCTTATGATGTCTATATCTTTCTT	350
Db	3232	TTTATATTTTATATATTTCTGCTGCT--TGTGAGGTGTGATGTGTCTATATCTTTCTT	3289
Qy	351	TCTTCTTTTGTGGTAGAATTTGATCTCTCAGCATTTGTCATCGTAGTCTTTCTTTT	410
Db	3590	TCTTCTTTTGTGGTAGAATTTGATCTCTCAGCATTTGTCATCGTAGTCTTTCTTTT	3349
Qy	411	CATGATTTGTGACAAATGCAGGCTCTGTCGGAGGCTTTTGTGAG	454
Db	3350	CATGATTTGTGACAAATGCAGGCTCTCTGTCGGAGGCTTTTGTGAG	3393

RESULT 15  
US-09-970-921-5  
; Sequence 5, Application US/09970921

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? APPLICANT: Frank Michiels et al
? TITLE OF INVENTION: Improved Barstar Gene
? FILE REFERENCE: 2428-0108P
? CURRENT APPLICATION NUMBER: US/09/970,921
? CURRENT FILING DATE: 2001-10-05
? NUMBER OF SEQ ID NOS: 10
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 5
? LENGTH: 4032
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: other nucleic
? OTHER INFORMATION: acid, "plasmid pmw71"
? NAME/KEY: misc_feature
? LOCATION: (1995)..(3400)
? OTHER INFORMATION: label = PRAC1, "promoter region of rice actin gene"
? OTHER INFORMATION: label = contains an intron in the leader"
? NAME/KEY: misc_feature
? LOCATION: (3401)..(3676)
? OTHER INFORMATION: label = barstar, "barstar DNA"
? NAME/KEY: misc_feature
? LOCATION: (3677)..(4003)
? OTHER INFORMATION: label = 3'nos, "region containing 3' untranslated
? OTHER INFORMATION: end of nopaline synthase gene of Agrobacterium
? OTHER INFORMATION: T-DNA"
? NAME/KEY: misc_feature
? LOCATION: (3399)..(3494)
? OTHER INFORMATION: label = NcoI, "NcoI recognition site"
? NAME/KEY: misc_feature
? LOCATION: (4015)..(4021)
? OTHER INFORMATION: label = KpnI, "KpnI recognition site"
? OS-09-970-921-5

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Best Local Similarity	93.1%	Pred. No. 1.6e-95		
Best 432; Conservative	0	Mismatches 20	Indels 12	Gaps 6

[illegible]

Oy	174	GCGGGAATGGGGCTCTCGATGAAATCT--GATCGCGCGTTTGGGGGAATGATG	231
Db	3112	GCGGGAATGGGGCTCTCGATGAAATCTGCGATCCGCGTTTGGGGGAATGATG	3171
Oy	232	GGCGTTAAATTT--GGCATGCTAAACAAGATAGGAAGGGGAAAAGGCACTATG	290
Db	3172	GGGGTTTAAATTTCCGCATGCTAAACAAGATAGGAAGGGGAAAAGGCACTATG	3211
Oy	291	TTTATTTTATATATTTCTGCTGCTCGTCAAGCTTAGATGTCTAGATCTTCTT	350
Db	3332	TTTATATTTTATATATTTCTGCTGCT--TGTGAGGCTTAGATGTCTAGATCTTCTT	3289
Oy	351	TCTTCTTTTGGGGTGAATTTGAATCCCTCAGCATTTGTCATCGTAGTTTCTTTT	410
Db	3290	TCTTCTTTTGGGGTGAATTTGAATCCCTCAGCATTTGTCATCGTAGTTTCTTTT	3349
Oy	411	CATGATTTGTACAATATGCAAGCTTCGTGGGAGCTTTTTTTGTAG	454
Db	3350	CATATTTGTACAATATGCAAGCTTCGTGGGAGCTTTTTTTGTAG	3393

Search completed: September 12, 2005, 04:00:33  
Job time : 75.0862 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using bw model

Run on: September 12, 2005, 02:27:12 ; Search time 578.125 Seconds  
(without alignments)  
5157.238 Million cell updates/sec

Title: US-10-758-799-2

Perfect score: 454  
Sequence: 1 GTAACACACCCGCCCCCTCTC.....CGTGCAGACTTTTGTGAG 454

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7351250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA.\*

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7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
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15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*  
19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq.\*  
20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq.\*  
21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq.\*  
22: /cgn2\_6/ptodata/1/pubpna/US10I\_NEW\_PUB.seq.\*  
23: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*  
24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	454	100.0	454	9	US-09-037-531-2
2	454	100.0	454	19	US-10-758-799-2
3	454	100.0	1565	9	US-09-037-531-3
4	454	100.0	1565	19	US-10-758-799-3
5	382.2	84.2	470	16	US-10-087-167-109
6	379.4	83.6	623	9	US-09-981-908-19
7	357.4	78.7	9359	21	US-10-344-977A-1

8	357.4	78.7	9359	22	US-10-344-975B-1	Sequence 1, Appli
9	355.8	78.4	491	9	US-09-376-940-50	Sequence 50, Appl
10	355.8	78.4	1597	22	US-10-839-092-50	Sequence 50, Appl
11	355.8	78.4	3034	20	US-10-841-796-34	Sequence 34, Appl
12	355.8	78.4	3039	15	US-10-232-665-19	Sequence 19, Appl
13	355.8	78.4	3039	15	US-10-232-665-21	Sequence 21, Appl
14	355.8	78.4	3044	15	US-10-232-665-18	Sequence 18, Appl
15	355.8	78.4	3450	15	US-10-232-665-17	Sequence 17, Appl
16	355.8	78.4	3455	15	US-10-232-665-36	Sequence 36, Appl
17	355.8	78.4	3469	15	US-10-232-665-23	Sequence 23, Appl
18	355.8	78.4	7794	24	US-11-057-062-1	Sequence 2, Appli
19	355.8	78.4	8590	24	US-11-057-062-1	Sequence 1, Appli
20	355.8	78.4	11546	20	US-10-841-796-33	Sequence 33, Appl
21	348	76.7	1384	22	US-10-839-092-35	Sequence 35, Appl
22	348	76.7	2480	21	US-10-678-588A-1	Sequence 1, Appli
23	348	76.7	4032	9	US-09-970-921-5	Sequence 5, Appli
24	348	76.7	5365	22	US-10-839-092-57	Sequence 57, Appl
25	348	76.7	6865	10	US-09-845-064-13	Sequence 13, Appl
26	348	76.7	7943	10	US-09-845-064-15	Sequence 15, Appl
27	348	76.7	9143	10	US-09-845-064-12	Sequence 12, Appl
28	348	76.7	10003	10	US-09-845-064-21	Sequence 21, Appl
29	348	76.7	10003	10	US-09-845-064-21	Sequence 21, Appl
30	346.4	76.3	4176	24	US-11-004-221-7	Sequence 7, Appli
31	338.4	74.5	2378	15	US-10-213-791-27	Sequence 27, Appl
32	338.4	74.5	8296	24	US-11-057-069-1	Sequence 1, Appli
33	290.2	63.9	2107	15	US-10-213-791-29	Sequence 29, Appl
34	290.2	63.9	2122	15	US-10-213-791-35	Sequence 25, Appl
35	203	44.7	1259	10	US-09-991-209-35	Sequence 43, Appl
36	203	44.7	4773	10	US-09-991-209-32	Sequence 32, Appl
37	203	44.7	4950	10	US-09-991-209-34	Sequence 34, Appl
38	203	44.7	4965	10	US-09-991-209-37	Sequence 37, Appl
39	203	44.7	4974	10	US-09-991-209-35	Sequence 35, Appl
40	203	44.7	5164	10	US-09-991-209-36	Sequence 36, Appl
41	203	44.7	5277	10	US-09-991-209-35	Sequence 25, Appl
42	203	44.7	5295	10	US-09-991-209-38	Sequence 38, Appl
43	203	44.7	5327	10	US-09-991-209-27	Sequence 27, Appl
44	203	44.7	5337	10	US-09-991-209-19	Sequence 19, Appl
45	203	44.7	5337	10	US-09-991-209-23	Sequence 23, Appl

#### ALIGNMENTS

RESULT 1  
US-09-037-531-2  
; Sequence 2, Application US/09037531  
; Patent No. US20020104117A1  
; GENERAL INFORMATION:  
; APPLICANT: Derose, Richard  
; TITLE OF INVENTION: Freysinet, Georges  
; TITLE OF INVENTION: Maize H3C4 Promoter Combined With The  
; TITLE OF INVENTION: First Intron Of Rice Actin, Chimeric Gene Comprising It  
; TITLE OF INVENTION: And Transformed Plant  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Connolly, Bove, Lodge, & Hutz  
; STREET: 1220 Market Street  
; CITY: Wilmington  
; STATE: DE  
; COUNTRY: USA  
; ZIP: 19899  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/037,531  
; FILING DATE: 10-MAR-1998  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMorow Jr., Robert G.  
; REGISTRATION NUMBER: 30962



RESULT 2  
 US-10-758-799-2  
 ; Sequence 2, Application US/10758799  
 ; Publication No. US20040199944A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DeRose, Richard  
 ; Freysainet, Georges  
 ; TITLE OF INVENTION: Maize H3C4 Promoter Combined With The  
 ; First Intron Of Rice Actin, Chimeric Gene Comprising It  
 ; And Transformed Plant  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Connolly, Bove, Lodge, & Hutz  
 ; STREET: 1220 Market Street  
 ; CITY: Wilmington  
 ; STATE: DE  
 ; COUNTRY: USA  
 ; ZIP: 19839  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
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: RESULT 3
: US-09-037-531-3
: Sequence 3, Application US/09037531
: Patent No. US20020104117A1
: GENERAL INFORMATION:
: APPLICANT: Derose, Richard
: APPLICANT: Freysinet, Georges
: TITLE OF INVENTION: Maize H3c4 Promoter Combined With The
: TITLE OF INVENTION: First Intron Of Rice Actin, Chimeric Gene Comprising It
: TITLE OF INVENTION: And Transformed Plant
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSES: Connolly, Bove, Lodge, & Hutz
: STREET: 1220 Market Street
:

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1 Sequence 1, Application US/103445975B
2 Publication No. US20050183172A1
3 GENERAL INFORMATION:
4 APPLICANT: Van der Valk, Pieter
5 APPLICANT: Van Dun, Cornelius M.P.
6 APPLICANT: Smeekens, Sijf C.M.
7 APPLICANT: Proveniers, Michael C.G.
8 TITLE OF INVENTION: Inhibition of Generative Propagation in Genetically Modified Heri
9 TITLE OF INVENTION: Resistant Grasses
10 PTE REFERENCE: ARNO120591
11 CURRENT APPLICATION NUMBER: US/10/344,975B
12 CURRENT FILING DATE: 2003-02-18
13 PRIOR APPLICATION NUMBER: PCT/EP01/09570
14 PRIOR FILING DATE: 2001-08-16
15 PRIOR APPLICATION NUMBER: US 60/226,422
16 PRIOR FILING DATE: 2000-08-18
17 NUMBER OF SEQ ID NOS: 4
18 SOFTWARE: PatentIn version 3.1
19 SEQ ID NO 1
20 LENGTH: 9359
21 TYPE: DNA
22 ORGANISM: Artificial Sequence
23 FEATURE:
24 OTHER INFORMATION: Vector pVDH636 nucleotide sequence
25 FEATURE:
26 NAME/KEY: gene
27 LOCATION: (839)..(1699)
28 OTHER INFORMATION: Beta-lactamase gene (Ampr)
29 FEATURE:
30 NAME/KEY: gene
31 LOCATION: (8085)..(9119)
32 OTHER INFORMATION: Hygromycin resistance gene from Escherichia coli
33 FEATURE:

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LOCATION: (9120) .. (9359)
OTHER INFORMATION: PolyA signal from 35S gene from Cauliflower mosaic virus
FEATURE:

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? LOCATION: (2941)..(4920)
? OTHER INFORMATION: Ubi-promoter from maize
?
? FEATURE:
? NAME/KEY: gene
? LOCATION: (4921)..(6400)
? OTHER INFORMATION: Ath1 gene from Arabidopsis thaliana
?
? FEATURE:
? NAME/KEY: polyA signal
? LOCATION: (6401)..(6672)
? OTHER INFORMATION: Poly-A signal from the nopaline synthetase gene from Agrobacterium tumefaciens
?
? OTHER INFORMATION: m tumefaciens
?
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: (7434)..(8084)
? OTHER INFORMATION: First exon-intron combination from Ubi-maize
?
? US-10-344-975B-1

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Query Match	78.7%	Score 357.4	DB 22	length 9359
Best Local Similarity	93.1%	Pred. No. 3.8e-95		
Matches 431	Conservative	0	Mismatches 21	Indels 11
				Gaps 5

Qy 1 GTATCACACCCGCCCCCTCCTCTCTTTCTTTCTCCGTTTTTTTTTGGTCCGCTCGAT 60

Dd 7624 GTATCACACCCGCCCCCTCCTCTCTTTCTTTCTCCGTTTTTTTTTGGTCCGCTCGAT 7683

Qy 61 CTTTGCGCTTGATGTTGGGTGGGCAGA-----GCGGCTTCGTCGCGCAGATCGGCGC 116

117 CCGGAGGGGGCGGATCTCCGGCTGCGCTCCG--GGCTGAGTCGSCCGGATCCCG 174



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;
; OTHER INFORMATION: cassette
;
; FEATURE:

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; SEQ ID NO 21

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1 LENGTH: 3039
2 TYPE: DNA
3 ORGANISM: Artificial Sequence
4 FEATURE:
5 OTHER INFORMATION: Description of Artificial Sequence: expression
6 OTHER INFORMATION: cassette
7 FEATURE:
8 NAME/KEY: Promoter
9 LOCATION: (14)..(235)
10 OTHER INFORMATION: P-CaMV.AS4
11 FEATURE:
12 NAME/KEY: 5'UTR
13 LOCATION: (240)..(304)
14 OTHER INFORMATION: L-Ta.hcb1
15 FEATURE:
16 NAME/KEY: Intron
17 LOCATION: (318)..(805)
18 OTHER INFORMATION: I-Os.Act1
19 FEATURE:
20 NAME/KEY: CDS
21 LOCATION: (811)..(2769)
22 OTHER INFORMATION: Cry3Bb1 variant 11231mw2
23 FEATURE:
24 NAME/KEY: terminator
25 LOCATION: (2787)..(3020)
26 OTHER INFORMATION: T-Ta.hspi7
27 US-10-232-665-21

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Query Match	78.4%;	Score 355.8;	DB 15;	Length 3039;
Best Local Similarity	92.9%;	Pred. No. 7e-96;		
Matches 430;	Conservative	0;	Mismatches 22;	Indels 11;
				Gaps 5;

OY	1	GTAAACCAACCCGCCCCCTCCGCTCTTTCCTTTCGCGTTTTTTTTTTTTTTCGTGGATCTCGAT	60
Dd	334	GTAAACCAACCCGCCCCCTCCGCTCTTTCCTTTCGTGGATCTCGAT	393
OY	61	CTTTGACCTTGATGTTTGAGTGAGGCGAGA----CGAGCTTCGTGCCCAAGTCGGTACG	116
Dd	394	CTTTGACCTTGATGTTTGAGTGAGGCGAGAGAGGCGGCTTCGTGCGGCCCAAGTCGGTACG	453
OY	117	CGGAGAGGGGCGGGAATCTCGCGGCTGGCGTCTCCG--GGCGTAGTCGGCCCGGATCTTCG	174
Dd	454	CGGAGAGGGGCGGGAATCTCGCGGCTGGCGGCTTCGCGCGGCGTAGATCGAGCCCGGATCTTCG	513
OY	175	CGGGGAATGGGGCTCTCGGATGTAGATGT--GATCCGCGGTGTGTGGGGAGATATGGG	232
Dd	514	CGGGGAATGGGGCTCTCGGATGTAGATGTCTCGCATTCGCCGTTGTTGGGGAGATATATGGG	573
OY	233	CGGTTTAAATTT--CGCAATGCTTAAACAAGATCAGAAAGGGGAAAGGCGCATATGCT	291
Dd	574	GGGTTTAAATTTTCGCGCGTGTCTTAAACAAGATCAGAAAGGGGAAAGGCGCATATGCT	633
OY	292	TTATATTTTATATATTTCTGTGCTGCTCGTCAGGCTTAGATGTCATGATCTTTCTTT	351
Dd	634	TTATATTTTATATATTTCTGTGCTGCT--TCGTCAGGCTTAGATGTCATGATCTTTCTTT	691
OY	352	CTTCTTTTGTGGGATGATTTTGAATTCCTCAGACATGTTCATCGATGATTTTCTTTTC	411
Dd	692	CTTCTTTTGTGGGATGATTTTGAATTCCTCAGACATGTTCATCGATGATTTTCTTTTC	751
OY	412	ATGATTTGTGCAAAATGCAAGCTCGTGCAGAGCTTTTTTTTGG	454
Dd	752	ATGATTTGTGCAAAATGCAAGCTCGTGCAGAGCTTTTTTTTGG	794

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RESULT 14
US-10-232-665-38
; Sequence 38, Application US/10232665
; Publication No. US20030115630A1
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn

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1 CURRENT APPLICATION NUMBER: US/10/232,665
2 CURRENT FILING DATE: 2002-08-29
3 PRIOR APPLICATION NUMBER: US/09/377,466
4 PRIOR FILING DATE: 1999-08-19
5 NUMBER OF SEQ ID NOS: 43
6 SOFTWARE: PatentIn Ver. 2.0
7 SEQ ID NO 38
8 LENGTH: 3044
9 TYPE: DNA
10 ORGANISM: Artificial Sequence
11 FEATURE:
12 OTHER INFORMATION: Description of Artificial Sequence: expression
13 OTHER INFORMATION: cassette
14 FEATURE:
15 NAME/KEY: promoter
16 LOCATION: (14)..(235)
17 OTHER INFORMATION: P-CamV.AS4
18 FEATURE:
19 NAME/KEY: 5'UTR
20 LOCATION: (240)..(304)
21 OTHER INFORMATION: L-Ta.hcb1
22 FEATURE:
23 NAME/KEY: intron
24 LOCATION: (318)..(805)
25 OTHER INFORMATION: I-Os.Act1
26 FEATURE:
27 NAME/KEY: CDS
28 LOCATION: (811)..(2769)
29 OTHER INFORMATION: variant Cry3Bb1 coding sequence encoding v11231
30 FEATURE:
31 NAME/KEY: terminator
32 LOCATION: (2792)..(3025)
33 OTHER INFORMATION: T-Ta.hsp17
34 US-10-232-665-38

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Query Match	78.4%;	Score 355.8;	DB 15;	Length 3044;
Best Local Similarity	92.9%;	Pred. No. 7e-96;		
Matches 430;	Conservative	0;	Mismatches 22;	Indels 11;
				Gaps 5

QY	1	GTAAACCAACCCGGCCCTCTCCCTCTTCTCTTCTCTCCGGTTTTTTTTTTCGGTCCGAT	60
Db	334	GTAAACCAACCCGGCCCTCTCCCTCTTCTCTCTCCGTTTTTTTTTTCGGTCTCGAT	393
QY	61	CTTTGGCCTTGTAATTTGGGTGGGCGAGA----GCGGCTTTCGTGCCAGATCGGTGCG	116
Db	394	CTTTGGCCTTGTAATTTGGGTGGGCGAGAGCGGCTTTCGTGCCGCCCAATCGGTGCG	453
QY	117	CGGGAGGGGGCGGGATCTTGCGGGCTGGCGTCTCCG--GGCTGATGTGGCCCGGATCCTCG	174
Db	454	CGGGAGGGGGCGGGATCTTGCGGGCTGGCGCGGTGGAATCCGACCGGATCTCG	513
QY	175	CGGGGAATGGGGCTCTCGATGTAGATCT--GATCCGCGTGTGTGGGGAGATGATGGG	232
Db	514	CGGGGAATGGGGCTCTCGATGTAGATCTCGGATTCGCCCTTGTGGGGAGATGATGGG	573
QY	233	GCGTTTAAATTT--CGCCATCTAAACAAGATCAGAAAGAGGAAAAAGGACATGAGT	291
Db	574	GCGTTTAAATTTCCGCCGTCTAAACAAGATCAGAAAGAGGAAAAAGGACATGAGT	633
QY	232	TTAATATTTTATATATTTCTGCTGCTGCTCGTCAAGCTTAAGATGCTAGATCTTTCTTT	351
Db	634	TTAATATTTTATATATTTCTGCTGCT--TCGTCAGGCTTAAGATGCTAGATCTTTCTTT	691
QY	352	CTTCTTTTGGGGAGATTTGGAATCCCTCAGACATTTGATCGGTAGTTTTCTTTTC	411
Db	692	CTTCTTTTGGGGAGATTTGGAATCCCTCAGACATTTTCAATCGTATGTTTTCTTTTC	751
QY	412	ATGATTTTGAACAATGCAAGCTCTGTCGAGCTTTTGTGAG	454
Db	752	ATGATTTTGAACAATGCAAGCTCTGTCGAGCTTTTGTGAG	794

## RESULT 15



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US-10-232-665-17
Sequence 17, Application US/10232665
Publication No. US20030115630A1
GENERAL INFORMATION:
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
CURRENT APPLICATION NUMBER: US/10/232,665
CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US/09/377,466
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 3450
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: expression
OTHER INFORMATION: cassette
FEATURE:
NAME/KEY: promoter
LOCATION: (14)..(235)
OTHER INFORMATION: P-CaMV_AS4
FEATURE:
NAME/KEY: 5'UTR
LOCATION: (240)..(304)
OTHER INFORMATION: L-Ta.hcb1
FEATURE:
NAME/KEY: intron
LOCATION: (318)..(805)
OTHER INFORMATION: I-Os.Act1
FEATURE:
NAME/KEY: transit_peptide
LOCATION: (825)..(971)
OTHER INFORMATION: amino terminal TS-Zm.rbcs
FEATURE:
NAME/KEY: intron
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OTHER INFORMATION: I-Zm.rbcs
FEATURE:
NAME/KEY: transit_peptide
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OTHER INFORMATION: carboxy terminus TS-Zm.rbcs
FEATURE:
NAME/KEY: CDS
LOCATION: (1222)..(3180)
OTHER INFORMATION: Cry3Bb1 variant 11231mv1
FEATURE:
NAME/KEY: terminator
LOCATION: (3198)..(3431)
OTHER INFORMATION: T-Ta.hsp17
US-10-232-665-17

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[illegible][illegible]

Search completed: September 12, 2005, 09:26:00  
Job time : 580.125 secs





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Db 421 GACAAATGACGCTCGTGGGAGCTTTTGTAG 454

RESULT 2  
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LOCUS Sequence 2 from patent US 6750378.  
DEFINITION AR559744  
ACCESSION AR559744 GI:53969842  
VERSION AR559744.1  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 454)  
AUTHORS Derose,R. and Freysbriet,G.  
TITLE Maize H3C4 promoter combined with the first intron of rice actin,  
chimeric gene comprising it and transformed plant  
JOURNAL Patent: US 6750378-A 2 15-JUN-2004;  
FEATURES  
source 1. .454  
Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 1.8e-246;  
Matches 454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAACACCCCGCCCTCTCTCTTTCTTCTCGTTTTTTTGGTCTCGGCTCGAT 60  
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QY 61 CTTTGGCTTGTAGTTTGGGTGGGCGAGACGCTTCTCGCCAGATCGTGGCGGG 120  
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Db 421 GACAAATGACGCTCGTGGGAGCTTTTGTAG 454

RESULT 3  
BD128390 454 bp DNA linear PAT 18-SEP-2002  
LOCUS BD128390  
DEFINITION Corn H3C4 promoter bonded to the first intron of rice actin,  
chimeric gene containing this promoter and transgenic plant.  
ACCESSION BD128390.1 GI:23223335  
VERSION JP 200250016-A/2.  
KEYWORDS unidentified  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 454)  
AUTHORS Durose,R. and Freysbriet,G.  
TITLE Corn H3C4 promoter bonded to the first intron of rice actin,  
chimeric gene containing this promoter and transgenic plant  
JOURNAL Patent: JP 200250016-A 2 08-JAN-2002;  
COMMENT AVENTIS CROPS SCIENCE SA  
OS unidentified  
PN JP 200250016-A/2  
PD 08-JAN-2002  
PF 22-DEC-1998 JP 2000526660  
PR 24-DEC-1997 FR 97/16726  
PI RICHARD DUROSE, GEORGES FREYSSIER  
PC C12N15/09,A01H5/00,C07K14/21,C07K14/415,C07K19/00,C12N5/10, PC  
C12Q1/68  
PC C12N15/00,C12N5/00  
CC Strandedness: Single;  
CC Topology: Linear;  
CC Corn H3C4 promoter bonded to the first intron of rice actin,  
chimeric gene  
CC containing this promoter and transgenic plant FH Key  
FT source 1. .454  
FT Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 1.8e-246;  
Matches 454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAACACCCCGCCCTCTCTCTTTCTTCTCGTTTTTTTGGTCTCGGCTCGAT 60  
Db 1 GTAACACCCCGCCCTCTCTCTTTCTTCTCGTTTTTTTGGTCTCGGCTCGAT 60  
QY 61 CTTTGGCTTGTAGTTTGGGTGGGCGAGACGCTTCTCGCCAGATCGTGGCGGG 120  
Db 61 CTTTGGCTTGTAGTTTGGGTGGGCGAGACGCTTCTCGCCAGATCGTGGCGGG 120  
QY 61 CTTTGGCTTGTAGTTTGGGTGGGCGAGACGCTTCTCGCCAGATCGTGGCGGG 120  
Db 61 CTTTGGCTTGTAGTTTGGGTGGGCGAGACGCTTCTCGCCAGATCGTGGCGGG 120  
QY 121 AGGGGCGGATCTCGCGGCTGGGCTCTCGGGGCTGAGTGGCCCGGATCCTGGCGGGA 180  
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QY 241 AATTGGCATGCTAAACAAGATCAGGAAGAGGGGAAAGGACATGCTATATATTTT 300  
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Db 301 TATATATTTCTGCTGCTGCTGCTCAGGCTTAGATGCTAGATCTTTCTTTCTTTT 360

LOCUS	Accession	Sequence	From patent	US 6750378.	linear	PAT 08-OCT-2004
DEFINITION	AR559745	Sequence 3	from patent	US 6750378.		
ACCESSION	AR559745					
VERSION	AR559745.1	GI:53969843				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	Unclassified.					
AUTHORS	1 (bases 1 to 1565)					
TITLE	Derose, R. and Freysinet, G.					
JOURNAL	Maize H3c4 promoter combined with the first intron of rice actin,					
FEATURES	chimeric gene comprising it and transformed plant					
SOURCE	Patent: US 6750378-A 3 15-JUN-2004;					
	Location/Qualifiers					
	1..1565					
ORIGIN	/organism="unknown"					
	/mol_type="genomic DNA"					
Query Match	100.0%;	Score 454;	DB 6;	Length 1565;		
Best Local Similarity	100.0%;	Pred. No. 1.9e-246;				
Matches 454;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
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DB	1102	GTAAACACACCCGGCCCTCTCCTCTTTTCTCTCGATTCTTTTGGTCTCGAT	1161			
QY	61	CTTTCGCTTGATGTTGGGTGGCGAGACGGCTTCGTCCAGATCGTGGCGGG	120			
DB	1162	CTTTTCGCTTGATGTTGGGTGGCGAGACGGCTTCGTCCAGATCGTGGCGGG	1221			
QY	121	AGGCGCGGAACTTCGCGGCTGGCGCTCTCCGCGCGTGAAGTCGCCGATCTCGCGGGA	180			
DB	1222	AGGCGCGGAACTTCGCGGCTGGCGCTCTCCGCGCGTGAAGTCGCCGATCTCGCGGGA	1281			
QY	181	ATGGGCGCTTCGGATGTAATCTGAATCCGCGCTTGTGGGGGAGATAGGGCGCTTAA	240			
DB	1282	ATGGGCGCTTCGGATGTAATCTGAATCCGCGCTTGTGGGGGAGATAGGGCGCTTAA	1341			
QY	241	AATTCGCGCATGCTAAACAAGATCAGGAGAGGGGAAAAGGCACTATGGTTATATTT	300			
DB	1342	AATTCGCGCATGCTAAACAAGATCAGGAGAGGGGAAAAGGCACTATGGTTATATTT	1401			
QY	301	TATATATTTCTGCTGCTGCTGCTCAGGCTTAGATGTGCTAGATCTTTCTTTCTTTT	360			
DB	1402	TATATATTTCTGCTGCTGCTGCTCAGGCTTAGATGTGCTAGATCTTTCTTTCTTTT	1461			
QY	361	GTGGGTGAATTTGAATCCCTCAGCATGTTTCATCGGTAGTTTCTTTTCAGATTTGT	420			
DB	1462	GTGGGTGAATTTGAATCCCTCAGCATGTTTCATCGGTAGTTTCTTTTCAGATTTGT	1521			
QY	421	GACAAATGCAGCCTCGGCGGAGACTTTTGTAG	454			
DB	1522	GACAAATGCAGCCTCGGCGGAGACTTTTGTAG	1555			
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LOCUS	BD128391	1565 bp	DNA	linear	PAT 18-SEP-2002	
DEFINITION	Corn H3c4 promoter bonded to the first intron of rice actin,					
ACCESSION	BD128391					
VERSION	BD128391.1	GI:23223336				
KEYWORDS	JP 2002500016-A/3.					
SOURCE	unidentified					
ORGANISM	unclassified.					
REFERENCE	1 (bases 1 to 1565)					
AUTHORS	DuRose, R. and Freysinet, G.					
TITLE	Corn H3c4 promoter bonded to the first intron of rice actin,					
JOURNAL	chimeric gene containing this promoter and transgenic plant					
	Patent: JP 2002500016-A 3 08-JAN-2002;					
	AVANTIS CROSCIENCE SA					

COMMENT	OS	Unidentified
	PN	JP 200250016-A/3
	PD	08-JAN-2002
	PF	22-DEC-1998 JR 2000526660
	PR	24-DEC-1997 FR 97/16726
	PI	RICHARD DUROSE, GEORGES PREYSSIER
	PC	C12N15/09, A01H5/00, C07K14/21, C07K14/415, C07K19/00, C12N5/10, PC
		C1201/68,
	PC	C12N15/00, C12N5/00
	CC	Strandedness: Single;
	CC	Topology: linear;
	CC	Corn H3C4 promoter bonded to the first intron of rice actin,
	CC	chimeric gene
	CC	containing this promoter and transgenic plant FH
	FT	Location/Qualifiers
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FEATURES		
source		

Query Match	100.0%	Score 454	DB 6	Length 1565
Best Local Similarity	100.0%	Pred. No.	1.9e-246	
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Db	1102	GTAAACCAACCGGCGCCCTCTCCCTCTTCTCTTCTTCCGTTTTTTTTTTCGTCGAGCTCGAT	1161
QY	61	CTTTGACCTTGATTTTGAGTGAGCGAGACGCGCTTTCGTGCGCCAGATCGATGCGCGG	120
Db	1162	CTTTGACCTTGATTTTGAGTGAGCGAGAGAGCGCTTTCGTGCGCCAGATCGATGCGCGG	1221
QY	121	AGGGGCGGGGATCTCGCGGCTGGCGTCTCCGGGCGTGAACTCGGCCCGGATCTCTCGCGGGGA	180
Db	1222	AGGGGCGGGGATCTCGCGGCTGGCGTCTCCGGGCGTGAACTCGGCCCGGATCTCTCGCGGGGA	1281
QY	181	ATGGGGCTCTCGAGTGTAGATCTGATTCGCGCGTGTGTTGGGGAGATGATGAGGCGTTTAA	240
Db	1282	ATGGGGCTCTCGAGTGTAGATCTGATTCGCGCGTGTGTTGGGGAGATGATGAGGCGTTTAA	1341
QY	241	AATTTCCGATGCTAAACAGATCAGAGAGGGGAAAAAGGCGACTATGCTTATATATTT	300
Db	1342	AATTTCCGATGCTAAACAGATCAGAGAGGGGAAAAAGGCGACTATGCTTATATATTT	1401
QY	301	TATATATTTCTGCGCTGCTGCTGCGAGCTTGATGTGCTAGATCTTTCTTTCTCTTTT	360
Db	1402	TATATATTTCTGCGCTGCTGCTGCGAGCTTGATGTGCTAGATCTTTCTTTCTCTTTT	1461
QY	361	GTGGGTAGAAATTTGAATCCCTCAGACATTTTCATCGTAGTATTTTCTTTTCATGATTTGT	420
Db	1462	GTGGGTAGAAATTTGAATCCCTCAGACATTTTCATCGTAGTATTTTCTTTTCATGATTTGT	1521
QY	421	GACCAATGACGCTCTGTGCGAGCTTTTTTTGAG 454	
Db	1522	GACCAATGACGCTCTGTGCGAGCTTTTTTTGAG 1555	

RESULT 7				
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LOCUS	AX467609	623 bp	DNA	linear
DEFINITION	Sequence 19 from Patent WO0234926.			
ACCESSION	AX467609			
VERSION	AX467609.1	GI:21900797		
KEYWORDS				
SOURCE				
ORGANISM	Oryza sativa			
	Oryza sativa			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.			

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REFERENCE
AUTHORS
TITLE
JOURNAL
Patent: WO 0234926-A 19 02-MAY-2002;
MICHIGAN STATE UNIVERSITY (US)
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				Gaps 0

OY	164	CCGGAATCTCCGGGGGAAATGGGGCTCTCGGATATGTAATCTGATCCGGCGTTGTTGGGGGA	223
Db	278	CCGAATCTCCGGGGGAATGGGGCTCTCGGATATGTAATCTGATCCGGCGTTGTTGGGGGA	337
OY	224	GATGATGCGGCGTTTAAATTTCCGCATGCTAAAAGAGATCAGAGAGGGGAAAAAGGC	283
Db	338	GATGATGCGGCGTTTAAATTTCCGCATGCTAAAAGAGATCAGGAAAGGGGAAAAAGGC	397
OY	284	ACATAGGTTAATTTTTTAATTTTCGCTCGCTCGTCAGGCTAAGATATGCTAAGAT	343
Db	398	ACATAGGTTAATTTTTTAATTTTCGCTCGCTCGTCAGGCTAAGATATGCTAAGAT	457
OY	344	CTTCTCTTCTCTTTTGGGTAGAAATTTGAATCCCTCAGACATGTTCTACGCTAGTTT	403
Db	458	CTTCTCTTCTCTTTTGGGTAGAAATTTGAATCCCTCAGACATGTTCTACGCTAGTTT	517
OY	404	TTCCTTTTCATGATTTGTGCAAAATCAGCCTCGTGGGAGCTTTTGTGTAG	454
Db	518	TTCCTTTTCATGATTTGTGCAAAATCAGCCTCGTGGGAGCTTTTGTGTAG	568

## RESULT

## VEAL LOCUS

## DEFINITION

## ACCESS

VERSION

## NETWORK SOURCE

ORGAN

**पञ्चमः**

## REFERENCE

TILL

1

JOUR  
MENT

**MEDUL  
PITUITARY**

## REFERENCE

AUTH:

TITLE

JOHN

## FEATURE

3

12

10

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Db	278	CCGAGTCTCGCGGGGAATGGGAGCTCGGAGTGTAGATCTGATCCGCGTGTGGGGGA	337
Qy	224	GATGATGGGGCGTTAAATTTCCGCGATCTMAACAAGTCAAGMAAGGGGAAAAGGCG	283
Db	338	GATGATGGGGCGTTAAATTTCCGCGATCTMAACAAGTCAAGMAAGGGGAAAAGGCG	397
Qy	284	ACTATGGTTATATTTTATATATTTCTGCTGCTGCTGTCAGGCTTGATGTGTAGAT	343
Db	398	ACTATGGTTATATTTTATATATTTCTGCTGCTGCTGTCAGGCTTGATGTGTAGAT	457
Qy	344	CTTTCCTTCTTCTTTTGTGGGAGAATTGAATCCCTACAGATTTGTCATCGTAGTTT	403
Db	458	CTTTCCTTCTTCTTTTGTGGGAGAATTGAATCCCTACAGATTTGTCATCGTAGTTT	517
Qy	404	TTTCCTTCATGATTTGTGACAAATGACGCGCTCGTGGGAGCGTTTGTGTAG	454
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RESULT 9
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LOCUS 150114 1392 bp DNA linear
DEFINITION Sequence 6 from patent US 5641876.
ACCESSION 150114
VERSION 150114.1 GI:2472334
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1392)
AUTHORS McElroy,D. and Wu,R.
TITLE Rice actin gene and promoter
JOURNAL Patent: US 5641876-A 6 24-JUN-1997;
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Qy	1196 ACTATGGTTATATTTTATATATTTTCGCTGCTGCTCAAGGCTTAGATGTGCTAGAT 1255
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Qy	1256 CTTCCTTCTCTTTTGTGGGTGAATTTGAATCCCTCAGACATTTGTTCATCGGTAGTTT 1315
Db	404 TTCTTTTCATGATTTGTGCAAAATGCAAGCTCTGTGCGAGCTTTTGTGTAG 454
Qy	1316 TTCTTTTCATGATTTGTGCAAAATGCAAGCTCTGTGCGAGCTTTTGTGTAG 1366

RESULT 10			
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ACCESSION	150115		PAT 07-OCT-1997
VERSION	150115.1	GI:2472335	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1404)		
AUTHORS	McElroy,D. and Wu,R.		
TITLE	Rice actin gene and promoter		
JOURNAL	Patent: US 5641876-A 7 24-JUN-1997;		
FEATURES	Location/Qualifiers		
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ORIGIN	Query Match	64.1%; Score 291; DB 6; Length 1404;
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	Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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QY	224 GATGATGGGGCGTTAAAAATTTCCCATGCTAAACAAGATCAGGAGAAGGGGAAAAGGC	283
Db	1146 GATGATGGGGCGTTAAAAATTTCCCATGCTAAACAAGATCAGGAGAAGGGGAAAAGGC	1205
QY	284 ACTATGGTTATATATTTTATATATATTTCTGCTGCTCGTCAGGCTTAGATGTGCTAGAT	343
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QY	344 CTTTCTTTCTTCTTTTGTGGGTGAAATTTGAATCCCTCAGCATTTGTATCGGTACTTT	403
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QY	404 TTTCTTTTCATGATTTTGACAAATGCAAGCCGCGGAGACCTTTTGTAG	454
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VERSION	I50113.1	GI:2472332						
KEYWORDS	.							
SOURCE	Unknown.							
ORGANISM	Unknown.							
REFERENCE	Unclassified. 1 (bases 1 to 2199)							
AUTHORS	Mcelroy,D. and Wu,R.							
TITLE	Rice actin gene and promoter							
JOURNAL	Patent: US 5641876-A 5 24-JUN-1997;							
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Best Local Similarity	100.0%;	Pred. No. 1.2e-153;						
Matches 291,	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;				
OY	164	CCGATCCTCGGGGAATTGGGGGCTCTCGAGTGTAGATCTGATCCGCCGTGTGGGGGA	223					
Db	1883	CCGATCCTCGGGGAATTGGGGGCTCTCGAGTGTAGATCTGATCCGCCGTGTGGGGGA	1942					
OY	224	GATGATGGGGCGTTAAAAATTTTCGCATGCTAAACAAGATCAGAGAAGGGGAAAAGGGC	283					
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Db	2003	ACTATGTTTTAATTTTAATAATTTTCGCTGCTGCTGCTCAAGCTTAGATGTGCTAGAT	2062					
OY	344	CTTCTCTTCTCTTTTTTGNGGAGAAATTGAATCCCTCACATTTTCATCGGTAGTT	403					
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OY	404	TTCTTTTCATGATTTTGACAATGCACCTCTGTGCGGAGCTTTTTTGTAG	454					
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ACCESSION	I50112							
VERSION	I50112.1	GI:2472332						
KEYWORDS	.							
SOURCE	Unknown.							
ORGANISM	Unknown.							
REFERENCE	Unclassified. 1 (bases 1 to 5643)							
AUTHORS	Mcelroy,D. and Wu,R.							
TITLE	Rice actin gene and promoter							
JOURNAL	Patent: US 5641876-A 4 24-JUN-1997;							
FEATURES	Location/Qualifiers . . .5643							
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OY	164	CCGATCCTCGGGGAATTGGGGGCTCTCGAGTGTAGATCTGATCCGCCGTGTGGGGGA	223					
Db	1886	CCGATCCTCGGGGAATTGGGGGCTCTCGAGTGTAGATCTGATCCGCCGTGTGGGGGA	1945					

Oy	22	GATGATGGGGCGTTTAAATTTGGCCATGCTAAACAAGATCAGAAAGGGAAGGCG	283
Db	1946	GATATATGGGGGTTTAAATTTGGCCATGCTAAACAAGATCAGAAAGGGAAGGCG	2005
Oy	284	ACTATGGTTATATTTTATATATTTCTGCTGCTGCTGTCAGGCTTAGATGTCTAGAT	343
Db	2006	ACTATGGTTATATTTTATATATTTCTGCTGCTGCTGTCAGGCTTAGATGTCTAGAT	2065
Oy	344	CTTTCTTTCTTTCTTTTGTGGGTAGAAATTGAATCCCTCAGCATTTTCATCGGTATTTT	403
Db	2066	CTTTCTTTCTTTCTTTTGTGGGTAGAAATTGAATCCCTCAGCATTTTCATCGGTATTTT	2125
Oy	404	TTCTTTTCATGATTTGTGACAAATGACGCCGCGGGAGACTTTTGTAG	454
Db	2126	TTCTTTTCATGATTTGTGACAAATGACGCCGCGGGAGACTTTTGTAG	2176
RESULT 13			
LOCUS	AK555357	470 bp	DNA
DEFINITION	Sequence 109 from Patent WO02061102.	linear	PAT 27-NOV-2002
ACCESSION	AK555357		
VERSION	AK555357.1	GI:25898876	
KEYWORDS			
SOURCE			
ORGANISM	Oryza sp.		
AUTHORS	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.		
REFERENCE	1	Pascal, E.J., Valentine, S.A., Brown, J.A., Cockrell, A.S. and Johnson, B.D.	
TITLE	Control of gene expression in plants		
JOURNAL	Patent: WO 02061102-A 109 08-AUG-2002; Syngenta Participations AG (CH)		
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Best Local Similarity	100.0%;	Pred. No. 1.5e-152;	Length 470;
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Gaps 0;			
Oy	166	GGATCCTCGCGGGGAATGGGGCTCTCGAGATGATCGATCCGCGTTGTTGGGGAGA	225
Db	166	GGATCCTCGCGGGGAATGGGGCTCTCGAGATGATCGATCCGCGTTGTTGGGGAGA	225
Oy	226	TGATGGGCGCTTTTAAATTTGCGCATGCTAAACAAGATCAGAAAGGGAAGGCGAC	285
Db	226	TGATGGGCGCTTTTAAATTTGCGCATGCTAAACAAGATCAGAAAGGGAAGGCGAC	285
Oy	286	TATGGTTATATTTTATATATTTCTGCTGCTGCTCGTCAAGCTTAAGTGTCTAGATCT	345
Db	286	TATGGTTATATTTTATATATTTCTGCTGCTGCTCGTCAAGCTTAAGTGTCTAGATCT	345
Oy	346	TTCTTTCTTTCTTTTGTGGGTAGAAATTGAATCCCTCAGCATTTTCATCGGTATTTT	405
Db	346	TTCTTTCTTTCTTTTGTGGGTAGAAATTGAATCCCTCAGCATTTTCATCGGTATTTT	405
Oy	406	CTTTTCATGATTTGTGACAAATGACGCTCGTGGAGCTTTTGTAG	454
Db	406	CTTTTCATGATTTGTGACAAATGACGCTCGTGGAGCTTTTGTAG	454
RESULT 14			
LOCUS	AK641982	1121 bp	DNA
DEFINITION	Sequence 15 from Patent WO02096192.	linear	PAT 21-FEB-2003
ACCESSION	AK641982		
VERSION	AK641982.1	GI:28474610	

KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE other sequences; artificial sequences.  
1 Werner, S., Marillonnet, S., Klimuk, V. and Gleba, Y.  
AUTHORS Process of producing environmentally safe transgenic organisms  
TITLE Patent: WO 02096192-A 15 05-DEC-2002;  
JOURNAL Icon Genetics AG (DE)  
FEATURES  
source  
1. 1121  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="3' fragment of synthetic CryIIIA gene preceeded by  
3' end of rice actin 1 intron flanked by HindIII and BamHI  
sites"

ORIGIN  
Query Match 45.8%; Score 208; DB 6; Length 1121;  
Best Local Similarity 100.0%; Pred. No. 2e-106;  
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 247 GCCATGCTAACAAGATCAGAGAGAGGAGGAGGACATGTTATATTTTATATA 306  
DB 7 GCCATGCTAACAAGATCAGAGAGGAGGAGGACATGTTATATTTTATATA 66  
QY 307 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 366  
DB 67 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 126  
QY 367 AGAATTTGAATCCCTCAGCATGTTTCATGCGTATGTTTCTTTTCATGATTGTGACAA 426  
DB 127 AGAATTTGAATCCCTCAGCATGTTTCATGCGTATGTTTCTTTTCATGATTGTGACAA 186  
QY 427 TGCAGCCTGCTGCGGAGCTTTTGTG 454  
DB 187 TGCAGCCTGCTGCGGAGCTTTTGTG 214

RESULT 15  
AY452735 4895 bp DNA circular SYN 19-DEC-2003  
LOCUS AY452735  
DEFINITION Reporter vector pActXN, complete sequence.  
ACCESSION AY452735  
VERSION AY452735.1 GI:39636979  
KEYWORDS  
SOURCE Reporter vector pActXN  
ORGANISM Reporter vector pActXN  
REFERENCE other sequences; artificial sequences; vectors.  
1 (bases 1 to 4895)  
AUTHORS Vickers, C.E., Xue, G.P. and Greshoff, P.M.  
TITLE A synthetic xylanase as a novel reporter in plants  
JOURNAL Plant Cell Rep. 22 (2), 135-140 (2003)  
MEDLINE 22867549  
PUBMED 12845475  
REFERENCE 2 (bases 1 to 4895)  
AUTHORS Vickers, C.E.  
TITLE Direct Submision  
JOURNAL Submitted (29-OCT-2003) ARC Centre for Integrative Legume Research,  
The University of Queensland, Room 213, John Hines Building (69),  
St. Lucia, Qld 4072, Australia  
FEATURES  
source  
1. 4895  
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267. .2274  
/note="sequence from cloning vector pBR322"  
468. .1328  
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DSPEELINAEIPIVNDERDITTPVAMATYTKLITGELITLASRQQLIDMEADKVGPL  
IRSAALPAGFIADKSGAGERSGRIIAALGPDKGSRIVIVITTSQATMDERNQIA  
EYCASLIKRM"  
2345. .2367  
misc\_feature  
/note="T7 RNA polymerase promoter"  
2426. .3338  
promoter  
/note="from rice actin gene; Act1"  
3339. .3792  
intron  
/note="intron 1 from rice actin gene; Act1"  
3800. .4513  
gene  
/gene="exYnA"  
3800. .4513  
CDS  
/gene="exYnA"  
/note="synthetic xylanase"  
/codon\_start=1  
/product="Xylanase"  
/protein\_id="AA29086.1"  
/db\_xref="GI:39636981"  
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ETFKQYFSVRQGRKRTSGHITVSDHFKEMAKQGMIGNLVYALNMGWSSGVADVTL  
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4535. .4872  
terminator  
/note="from rbcS gene"  
4895  
misc\_feature  
/note="SP6 RNA polymerase transcription initiation site"

ORIGIN  
Query Match 44.9%; Score 204; DB 12; Length 4895;  
Best Local Similarity 100.0%; Pred. No. 4.1e-104;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTAACACCCCGCCCT 60  
DB 3339 GTAACACCCCGCCCT 3398  
QY 61 CTTTGCCCTTGGATGTTGGGTGGGCGAGAGCGGCTTCTCCGCCAGATCGGTGCCGGG 120  
DB 3399 CTTTGCCCTTGGATGTTGGGTGGGCGAGAGCGGCTTCTCCGCCAGATCGGTGCCGGG 3458  
QY 121 AGGGGCGGAGATCTCGGCGCTGGGCGTCTCGGGGCGTGAATCGGCGCGGATCTCGCGGGGA 180  
DB 3459 AGGGGCGGAGATCTCGGCGCTGGGCGTCTCGGGGCGTGAATCGGCGCGGATCTCGCGGGGA 3518  
QY 181 ATGGGCTCTCGGATGATGATCTG 204  
DB 3519 ATGGGCTCTCGGATGATGATCTG 3542

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
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Title: US-10-758-799-2

Perfect score: 454  
Sequence: 1 GTAAACCAACCCGCCCTCTC.....CGTGGAGCTTTTGTAG 454

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: Geneseq\_16Dec04:\*  
2: geneseqn19808:\*  
3: geneseqn19908:\*  
4: geneseqn20008:\*  
5: geneseqn20018:\*  
6: geneseqn20028:\*  
7: geneseqn20038:\*  
8: geneseqn20048:\*  
9: geneseqn20058:\*  
10: geneseqn20068:\*  
11: geneseqn20078:\*  
12: geneseqn20088:\*  
13: geneseqn20098:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	454	100.0	454	AAZ91038	Aaz91038 Rice acti
2	454	100.0	1565	AAZ91039	Aaz91039 Chimeric
3	291	64.1	623	AAZ47117	Aaz47117 Rice Acti
4	291	64.1	623	ABK86738	ABK86738 Rice Acti
5	291	64.1	1392	AAT80053	Aat80053 Rice acti
6	291	64.1	2199	AAT80052	Aat80052 Rice acti
7	291	64.1	5643	AAT80055	Aat80055 Rice acti
8	289	63.7	470	ABT07357	ABT07357 Reporter
9	289	63.7	470	ADF49181	ADF49181 Rice acti
10	208	45.8	1121	ABZ70926	Abz70926 CytIIIA 3
11	204	44.9	13680	ADP73931	Adp73931 Plasmid p
12	203	44.7	1259	ADG69912	Adg69912 Actin pro
13	203	44.7	1259	ADN88926	Adn88926 Actin pro
14	203	44.7	3657	ADG68992	Adg68992 Vector pr
15	203	44.7	4604	ADG68905	Adg68905 Vector pr
16	203	44.7	4773	ADG68901	Adg68901 Vector pr
17	203	44.7	4773	ADN88915	Adn88915 pGTV vect
18	203	44.7	4950	ADG68903	Adg68903 Vector pr
19	203	44.7	4950	ADN88917	Adn88917 pD06.1 ve
20	203	44.7	4965	ADG68906	Adg68906 Vector pr

#### ALIGNMENTS

21	203	44.7	4974	6	ADG69904	Adg69904 Vector pr
22	203	44.7	4974	11	ADN88918	Adn88918 pD04 vect
23	203	44.7	5164	11	ADN88919	Adn88919 pD01.1 v
24	203	44.7	5267	11	ADN88907	Adn88907 pTP8-5 ve
25	203	44.7	5277	6	ADG68994	Adg68994 Vector pr
26	203	44.7	5277	11	ADN88909	Adn88909 pTP5-1 ve
27	203	44.7	5295	6	ADG69907	Adg69907 Vector pr
28	203	44.7	5295	11	ADN88922	Adn88922 pD04 vect
29	203	44.7	5327	6	ADG69886	Adg69886 Vector pr
30	203	44.7	5337	11	ADN88911	Adn88911 pTP42 ve
31	203	44.7	5337	6	ADG69888	Adg69888 Vector pr
32	203	44.7	5337	6	ADG69900	Adg69900 Vector pr
33	203	44.7	5337	11	ADN88914	Adn88914 pTP5 vect
34	203	44.7	5337	11	ADN88903	Adn88903 pTP4 vect
35	203	44.7	5338	6	ADG69884	Adg69884 Vector pr
36	203	44.7	5338	6	ADG69898	Adg69898 Vector pr
37	203	44.7	5338	11	ADN88913	Adn88913 pTP3-1 ve
38	203	44.7	5338	11	ADN88899	Adn88899 pTP10-1 v
39	203	44.7	5345	6	ADG69886	Adg69886 Vector pr
40	203	44.7	5345	11	ADN88901	Adn88901 pTP4-4 ve
41	203	44.7	5387	6	ADG69910	Adg69910 Vector pr
42	203	44.7	5387	11	ADN88925	Adn88925 pTP1-1 v
43	203	44.7	5395	6	ADG69890	Adg69890 Vector pr
44	203	44.7	5395	11	ADN88905	Adn88905 pTP5.14 v
45	203	44.7	5510	2	AAQ12707	Aaq12707 Rice acti

RESULT 1  
AAZ91038 standard; DNA; 454 BP.

ID	AAZ91038	standard; DNA; 454 BP.
XX	AAZ91038;	
AC		
XX		
DT	06-JUN-2000	(first entry)
XX		
DE		Rice actin gene intron 1 sequence.
XX		
KM		Regulatory element; monocotyledonous vegetable plant cell; maize;
KW		histone H3C4; promoter; rice actin gene intron; chimeric; ss;
KW		herbicide resistance.
XX		
OS		Oryza sativa.
XX		
PN	FR2772787-AL.	
XX		
PD	25-JUN-1999.	
XX		
PF	24-DEC-1997;	97FR-00016726.
XX		
PR	24-DEC-1997;	97FR-00016726.
XX		
PA	(RHON ) RHONE-POULENC AGROCHIMIE.	
XX		
PI	Derose R. Freyssinet G;	
XX		
DR	WPI; 1999-397352/34.	
PT	5' chimeric regulatory region comprising maize histone H3C4 promoter and	
XX	rice actin gene first intron.	
PS	Claim 5; Page 14; 24pp; French.	
CC	The invention relates to a DNA sequence (AAZ91039) comprising a 5'	
CC	regulatory element for the expression of a heterologous gene in a	
CC	monocotyledonous vegetable plant cell. The DNA comprises: (a) a	
CC	functional fragment of the maize histone H3C4 promoter sequence	
CC	(AAZ91037); and (b) a functional fragment of the first intron of the rice	
CC	actin gene (this sequence). The chimeric regulatory region is useful for	
CC	the expression of heterologous genes that confer resistance to certain	
CC	herbicides, or that have novel agronomical properties in monocotyledons.	



Key	Location/Qualifiers
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FT	/*tag= a
FT	42..120
FT	/*tag= c
FT	/note= "Fragment of Act1 exon 1"
FT	42
FT	/*tag= b
FT	/note= "transcriptional start site for Act1 gene"
FT	121..568
FT	/*tag= d
FT	/note= "act1 intron"
FT	569..623
FT	/*tag= e
FT	576..623
FT	/*tag= f
FT	/product= "N-terminal 16 amino acids of GUS protein"
PN	
XX	MO958644-A1.
PD	
XX	18-NOV-1999.
XX	
PF	13-MAY-1999; 99MO-US010576.
XX	
PR	14-MAY-1998; 98US-00078862.
XX	
PA	(UYHA-) UNIV HAMAIL.
XX	
PI	Nan G, Nagai C;
DR	WPI: 2000-062292/05.
DR	P-PSDB; AAY56018.
XX	
PT	
XX	
PS	
XX	
CC	Example 2; Fig 3; 87pp; English.
CC	The invention relates to the generation of a stably transformed
CC	transgenic pineapple-like totipotent body. The methods are used for the
CC	production of transgenic pineapple-like totipotent bodies, and in
CC	particular, transgenic plants derived from them. The plants can be
CC	engineered to exhibit resistance to pests and disease and to exhibit
CC	improved qualities. The transgenic bodies can be transformed with
CC	constructs containing genes of interest as the maize sucrose phosphate
CC	synthase enzyme (GenBank accession m97550) or a sweetness protein (e.g.
CC	thaumatin) to increase the sweetness of the fruit. Alternatively,
CC	constructs can include antisense sequences to inhibit gene expression,
CC	e.g. an antisense construct to ACC synthase, which would delay fruit
CC	ripening or to polyphenol oxidase (GenBank accession s40548) which would
CC	prevent the browning reaction occurs during chilling injury. The
CC	expression constructs comprises promoter which drives the expression of
CC	the gene of interest. This sequence represents an example of a construct
CC	and comprises the 5' transcribed region of the rice actin-1 gene linked
CC	to the beta-glucuronidase enzyme coding sequence
XX	
SQ	Sequence 623 BP; 98 A; 184 C; 164 G; 177 T; 0 U; 0 Other;
Query Match	64.1%; Score 291; DB 3; Length 623;
Best Local Similarity	100.0%; Pred. No. 2e-130;
Matches 291; Conservative	0; Mismatches 0; Indels 0; Gaps 0
164	CCGGAATCTTCGCGGGAATGAGGCTTCGGAATGATGATTCGATCCGCGTGTGGGAGGA 223
278	CCGGAATCTTCGCGGGAATGAGGCTTCGGAATGATGATTCGATCCGCGTGTGGGAGGA 337

OY	224	GATGATGGGGCGCTTTAAATTTCCGCAATGCTTAACAAATGATCAGAGAGGGGAAAAAGGCG	263
DB	338	GATGATGGGGCGCTTTAAATTTCCGCAATGCTTAACAAATGATCAGAGAGGGGAAAAAGGCG	397
OY	284	ACTATGGTTTATTTTATTTATTTTCGCTGCTGCTGTGAGGCTTAGATGTCTGAT	343
OY	398	ACTATGGTTTATTTTATTTATTTTCGCTGCTGCTGTGAGGCTTAGATGTCTGAT	457
DB	344	CTTTCCTTCTCTTTTGTGGGTAGAAATTGAAATCCCTCAGCAATGTCATCGGTAGTTT	403
OY	458	CTTTCCTTCTCTTTTGTGGGTAGAAATTGAAATCCCTCAGCAATGTCATCGGTAGTTT	517
DB	404	TTCTTTTCATGATTTGTGCAAAATGACGCTCTGTGCGGAGCTTTTGTAG	454
	518	TTCTTTTCATGATTTGTGCAAAATGACGCTCTGTGCGGAGCTTTTGTAG	568
RESULT 4			
ABK86738	ABK86738 standard, DNA, 623 BP.		
AC	ABK86738;		
XX	24-SEP-2002 (first entry)		
DT	Rice Act1 gene.		
XX	Rice; gene; ds; transgenic; plant; lignocellulose; cellulase; ligninase;		
KW	Fermentable sugar; ethanol; fermentation; silage; feed; fuel;		
KW	industrial chemical; biodegradation; chloroaromatic;		
KM	environmental pollutant; Act1.		
XX	Oryza sativa.		
OS	MO200234926-A2.		
XX	02-MAY-2002.		
PD	18-OCT-2001; 2001WO-US032538.		
XX	20-OCT-2000; 2000US-0242408P.		
PF	(UNMS ) UNIV MICHIGAN STATE.		
XX	Sticklen MB, Dale BG, Magpool S;		
PI	WPI; 2002-489947/52.		
XX	Producing transgenic plants which after harvest degrade lignin and		
PT	cellulose to fermentable sugars, by mating transgenic plant comprising		
PT	DNA encoding cellulase with transgenic plant comprising		
PT	ligninase.		
XX	Example 1; Page 124; 126pp; English.		
XX	The invention discloses the production of a transgenic plant which		
CC	degrades lignocellulose when the plant is ground. It comprises the		
CC	production of the transgenic plant including cellulase and ligninase by		
CC	mating a transgenic plant, containing a DNA encoding a cellulase, and a		
CC	transgenic plant, containing a DNA encoding a ligninase, where both genes		
CC	are operably linked to a nucleotide sequence encoding a signal peptide		
CC	which targets the fusion protein to an organelle of the plant,		
CC	particularly chloroplasts. The method is useful for producing a		
CC	transgenic plant (e.g. maize) which degrades lignocellulose when the		
CC	plant is ground to produce a plant material. This material is useful for		
CC	converting lignocellulose, in a plant material, to fermentable sugars		
CC	which are then fermented to ethanol. The transgenic plants also provide a		
CC	plentiful and inexpensive source of fungal or bacterial cellulases and		
CC	ligninases which can be used in the production of ethanol. They can also		
CC	be used for pre-treating silage to increase the energy value of		
CC	lignocellulosic feeds for cows and other ruminant animals, pre-treating		
CC	lignocellulosic biomass for fermentative conversion to fuels and		

CC	industrial chemicals, and biodegradation of chloroaromatic environmental
CC	pollutants. The sequence presented is the rice Act1 gene and promoter
XX	
SQ	Sequence 623 BP; 98 A; 184 C; 164 G; 177 T; 0 U; 0 Other;
<hr/>	
Query Match	64.1%; Score 291; DB 6; Length 623;
Best Local Similarity	100.0%; Pred. No. 2e-130;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	164 CCGATGCTCGGGGAATAGGAGCCTCGAGTATGATCGATCCGCCGTGTGGGGGA 223
Db	278 CCGATTCCTCGGGGAATAGGAGCCTCGAGTATGATCGATCCGCCGTGTGGGGGA 337
OY	224 GATGATGGGGCGTTTAAATTTCGCACATCTAACAAGATCAGAGAAGGGAAAAAGGC 283
Db	338 GATGATGGGGCGTTTAAATTTCGCACATCTAACAAGATCAGAGAAGGGAAAAAGGC 397
OY	284 ACTATGCTTATATTTTTATATTTCTGCTGCTGCTGCTGCAAGCTTAATGTGCTAGAT 343
Db	398 ACTATGCTTATATTTTTATATTTCTGCTGCTGCTGCTGCAAGCTTAATGTGCTAGAT 457
OY	344 CTTCCTTCTCTTTTGTGGGATGAAATCCCTGAGCATTTGTCATCGTAGTTT 403
Db	458 CTTCCTTCTCTTTTGTGGGATGAAATCCCTGAGCATTTGTCATCGTAGTTT 517
OY	404 TTCTTTTCATGATTTGTGACAAATGACGCTCTGTGCGAGCTTTTGTGAG 454
Db	518 TTCTTTTCATGATTTGTGACAAATGACGCTCTGTGCGAGCTTTTGTGAG 568
<hr/>	
RESULT 5	
AAT80053	
ID	AAT80053 strand; cDNA; 1392 BP.
XX	
AC	AAT80053;
XX	
DT	25-MAR-2003 (revised)
DT	04-NOV-1997 (first entry)
XX	
DE	Rice actin 1 gene promoter fragment.
XX	
KM	Promoter; rice; actin 1 gene; cytoplasm; cytoskeleton; extension growth;
KX	cytoplasmic streaming; cell division; Rac1; maize; Adhl promoter; ss.
XX	
OS	Oryza sativa.
XX	
PN	US5641876-A.
PD	
XX	24-JUN-1997.
XX	
PF	27-OCT-1993; 93US-00144602.
XX	
PR	05-JAN-1990; 90US-00461490.
PR	18-SEP-1991; 91US-00762680.
XX	
PA	(CORR ) CORNELL RES FOUND INC.
XX	
PI	Wu R, McElroy D;
DR	WPT; 1997-340996/31.
XX	
PT	Nucleic acid containing the promoter of the rice actin-1 gene - used to
XX	direct efficient expression of foreign genes in rice.
PS	Claim 4; Col 35-38; 29pp; English.
XX	
CC	This sequence represents a fragment from the promoter region of the rice
CC	actin-1 (Rac1) gene. Cytoplasmic actin is a fundamental and essential
CC	component of the eukaryotic cell and cytoskeleton. In higher plant cells,
CC	a number of cellular processes, such as cytoplasmic streaming, extension
CC	growth and cell division are thought to involve the cytoskeletal actin
CC	protein. All of the studied plant actins consist of four exons of
CC	conserved length, separated by 3 introns of variable length. In rice

Query Match	64.1%	Score 291	DB 2	Length 1392
Best Local Similarity	100.0%	Pred. No. 2.1e-130		
Matches 291	Conservative 0	Mismatches 0	Indels 0	Gaps 0
CC	there are at least 8 actin-like sequences per haploid genome. Rac1			
CC	encodes a transcript that is relatively abundant in all rice tissues.			
CC	This sequence is an example of a nucleic acid molecule of the invention.			
CC	The nucleic acid molecules of the invention contain the Rac1 gene (or			
CC	fragments) with promoter activity in monocotyledonous plants. The			
CC	promoter is used to direct expression of foreign genes in transgenic rice			
CC	and other plants. The actin promoter is more efficient in rice			
CC	transformation than previously proposed promoters (e.g. 5 times more			
CC	active than the maize Adh1 promoter) and has constitutive activity in			
CC	space and time. (Updated on 25-MAR-2003 to correct PF field.)			
XX				
SO	Sequence 1392 BP; 376 A; 343 C; 309 G; 364 T; 0 U; 0 Other;			
QY	164	CCGGATCCTCGCGGGGAATGGGGCTCTCGGATGAGATCGATCCGCGTTGTTGGGGGA	223	
DB	1076	CCGGATCCTCGCGGGGAATGGGGCTCTCGGATGAGATCGATCCGCGTTGTTGGGGGA	1135	
QY	224	GATGATGGGGCGTTAAATTTCCCATGCTAAACAAGATCAGAGAAGGGAAAGGCG	283	
DB	1136	GATGATGGGGCGTTAAATTTCCCATGCTAAACAAGATCAGAGAAGGGAAAGGCG	1195	
QY	284	ACTATGTTTAAATTTTAAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAT	343	
DB	1196	ACTATGTTTAAATTTTAAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAT	1255	
QY	344	CTTCTCTTCTCTTTTGTGGTGAATTTGAATCCCTCAGCATTTGTCATCGTAACTT	403	
DB	1256	CTTCTCTTCTCTTTTGTGGTGAATTTGAATCCCTCAGCATTTGTCATCGTAACTT	1315	
QY	404	TTCTTTTCATGATTTTGACAATATGACAGCCCTGTCGAGAGCTTTTGTGATG	454	
DB	1316	TTCTTTTCATGATTTTGACAATATGACAGCCCTGTCGAGAGCTTTTGTGATG	1366	
RESULT 6				
AAT80052				
ID	AAT80052 standard; cDNA; 2199 BP.			
AC	AAT80052;			
XX				
DT	25-MAR-2003 (revised)			
DT	04-NOV-1997 (first entry)			
XX				
DE	Rice actin 1 gene promoter region.			
XX				
KM	Promoter; rice; actin 1 gene; cytoplasm; cytoskeleton; extension growth;			
KW	Cytoplasmic streaming; cell division; Rac1; maize; Adh1 promoter; ss.			
XX				
OS	Oryza sativa.			
XX				
PN	US641876-A.			
XX				
PD	24-JUN-1997.			
XX				
PF	27-OCT-1993; 93US-0014602.			
XX				
PR	05-JAN-1990; 90US-00461490.			
XX	18-SEP-1991; 91US-00762680.			
PA	(CORR ) CORNELL RES FOUND INC.			
PI				
PI	Wu R, Mcelroy D;			
XX				
DR	WPI; 1997-340996/31.			
PT	Nucleic acid containing the promoter of the rice actin-1 gene - used to			
XX	direct efficient expression of foreign genes in rice.			
PS	Claim 3; Col 33-36; 29pp; English.			



```
XX CC This sequence represents the promoter region from the rice actin-1 (Rac1)
CC gene. Cytoplasmic actin is a fundamental and essential component of the
CC eukaryotic cell and cytoskeleton. In higher plant cells, a number of
CC cellular processes, such as cytoplasmic streaming, extension growth and
CC cell division are thought to involve the cytoskeletal actin protein. All
CC of the studied plant actins consist of four exons of conserved length.
CC separated by 3 introns of variable length. In rice there are at least 8
CC actin-like sequences per haploid genome. Rac1 encodes a transcript that
CC is relatively abundant in all rice tissues. This sequence is an example
CC of a nucleic acid molecule of the invention. The nucleic acid molecules
CC of the invention contain the Rac1 gene (or fragments) with promoter
CC activity in monocotyledonous plants. The promoter is used to direct
CC expression of foreign genes in transgenic rice and other plants. The
CC actin promoter is more efficient in rice transformation than previously
CC proposed promoters (e.g. 5 times more active than the maize Adh1
CC promoter) and has constitutive activity in space and time. (Updated on 25
CC -MAR-2003 to correct PF field.)
XX SQ Sequence 2199 BP; 603 A; 515 C; 446 G; 635 T; 0 U; 0 Other;
Query Match 64.1%; Score 291; DB 2; Length 2199;
Best Local Similarity 100.0%; Pred. No. 2.1e-130;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 164 CCGGATCTTCGCGGGGAATGGGCTCTCGAGTGTAGATCGCCGTTGTTGGGGGA 223
DB 1883 CCGGATCTTCGCGGGGAATGGGCTCTCGAGTGTAGATCGCCGTTGTTGGGGGA 1942
QY 224 GATGATGGGGCGTTAAATTTGSCCATGCTAAACAAGATCAGAGGGAAGGGAAGGGC 283
DB 1943 GATGATGGGGCGTTAAATTTGSCCATGCTAAACAAGATCAGAGGGAAGGGAAGGGC 2002
QY 284 ACTATGTTTAAATTTTATATATTTCTGCTGCTGCTCAGGCTTAGATGTGCTAGAT 343
DB 2003 ACTATGTTTAAATTTTATATATTTCTGCTGCTGCTCAGGCTTAGATGTGCTAGAT 2062
QY 344 CTTTCTTTCTTTCTTTTGTGGGTAGAAATTTGAATCCTCAGACTTGTTCATCGGTAGTT 403
DB 2063 CTTTCTTTCTTTCTTTTGTGGGTAGAAATTTGAATCCTCAGACTTGTTCATCGGTAGTT 2122
QY 404 TTTCTTTTCATGATTTTGACAAATGACGCTCGGCGGAGCTTTTGTGAG 454
DB 2123 TTTCTTTTCATGATTTTGACAAATGACGCTCGGCGGAGCTTTTGTGAG 2173
RESULT 7
AAT80055
ID AAT80055 standard; cDNA; 5643 BP.
XX AC AAT80055;
XX DT 25-MAR-2003 (revised)
XX DT 04-NOV-1997 (first entry)
XX DE Rice actin 1 gene.
XX KM Promoter; rice; actin 1 gene; cytoplasm; cytoskeleton; extension growth;
XX KM cytoplasmic streaming; cell division; Rac1; maize; Adh1 promoter; ss.
XX OS Oryza sativa.
XX PN US5641876-A.
XX PD 24-JUN-1997.
XX PF 27-OCT-1993; 93US-00144602.
XX PR 05-JAN-1990; 90US-00461490.
XX PR 18-SEP-1991; 91US-00762680.
XX PA (CORR ) CORNELL RES FOUND INC.
```

```
PI Wu R, Mcelroy D;
XX DR WPI; 1997-340996/31.
XX PT Nucleic acid containing the promoter of the rice actin-1 gene - used to
XX PT direct efficient expression of foreign genes in rice.
XX PS Example 1; Col 3-7; 29pp; English.
XX CC This sequence represents a the rice actin-1 (Rac1) gene amplified using
CC AAT80054. Cytoplasmic actin is a fundamental and essential component of
CC the eukaryotic cell and cytoskeleton. In higher plant cells, a number of
CC cellular processes, such as cytoplasmic streaming, extension growth and
CC cell division are thought to involve the cytoskeletal actin protein. All
CC of the studied plant actins consist of four exons of conserved length,
CC separated by 3 introns of variable length. In rice there are at least 8
CC actin-like sequences per haploid genome. Rac1 encodes a transcript that
CC is relatively abundant in all rice tissues. This sequence is an example
CC of a nucleic acid molecule of the invention. The nucleic acid molecules
CC of the invention contain the Rac1 gene, or fragments with promoter
CC activity (see AAT80052 and AAT80053) in monocotyledonous plants. The
CC promoter is used to direct expression of foreign genes in transgenic rice
CC and other plants. The actin promoter is more efficient in rice
CC transformation than previously proposed promoters (e.g. 5 times more
CC active than the maize Adh1 promoter) and has constitutive activity in
CC space and time. (Updated on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 5643 BP; 1500 A; 1283 C; 1200 G; 1660 T; 0 U; 0 Other;
Query Match 64.1%; Score 291; DB 2; Length 5643;
Best Local Similarity 100.0%; Pred. No. 2.1e-130;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 164 CCGGATCTTCGCGGGGAATGGGCTCTCGAGTGTAGATCGCCGTTGTTGGGGGA 223
DB 1886 CCGGATCTTCGCGGGGAATGGGCTCTCGAGTGTAGATCGCCGTTGTTGGGGGA 1945
QY 224 GATGATGGGGCGTTAAATTTGSCCATGCTAAACAAGATCAGAGGGAAGGGAAGGGC 283
DB 1946 GATGATGGGGCGTTAAATTTGSCCATGCTAAACAAGATCAGAGGGAAGGGAAGGGC 2005
QY 284 ACTATGTTTAAATTTTATATATTTCTGCTGCTGCTCAGGCTTAGATGTGCTAGAT 343
DB 2006 ACTATGTTTAAATTTTATATATTTCTGCTGCTGCTCAGGCTTAGATGTGCTAGAT 2065
QY 344 CTTTCTTTCTTTTGTGGGTAGAAATTTGAATCCTCAGACTTGTTCATCGGTAGTT 403
DB 2066 CTTTCTTTCTTTTGTGGGTAGAAATTTGAATCCTCAGACTTGTTCATCGGTAGTT 2125
QY 404 TTTCTTTTCATGATTTTGACAAATGACGCTCGGCGGAGCTTTTGTGAG 454
DB 2126 TTTCTTTTCATGATTTTGACAAATGACGCTCGGCGGAGCTTTTGTGAG 2176
RESULT 8
ABT07357
ID ABT07357 standard; DNA; 470 BP.
XX AC ABT07357;
XX DT 07-NOV-2002 (first entry)
XX DE Reporter construct fragment rice actin intron SEQ ID NO: 109.
XX KM Plant; gene expression control; insect; hormone receptor; fertility;
XX KM ecdysone receptor; ds.
XX OS Oryza sativa.
XX PN WO200261102-A2.
XX PD 08-AUG-2002.
```

PF	24-OCT-2001; 2001MO-US051417.
XX	
FR	24-OCT-2000; 2000US-0242969P.
XX	
PA	(SYGN ) SYNGENTA PARTICIPATIONS AG.
PI	Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX	
DR	WP1; 2002-619259/66.
XX	
PT	New receptor cassette encoding a chimeric receptor polypeptide, useful in
PT	regulating expression of target polypeptides in plants in the presence of
PT	appropriate ligands that may be used in controlling plant fertility.
XX	
PS	Example 10; Page 263; 319pp; English.
XX	
CC	The present invention relates to a receptor cassette encoding a chimeric
CC	receptor polypeptide comprising at least one DNA binding domain, a hinge
CC	domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
CC	domain of an insect ECR, where the ligand binding domain is heterologous
CC	with respect to the hinge domain and an activation domain. The chimeric
CC	insect hormone receptors and receptor cassettes are useful in regulating
CC	expression of target polypeptides in plants in the presence of
CC	appropriate ligands that may be used in controlling plant fertility. The
CC	method is useful for decreasing or increasing plant gene expression. The
CC	present sequence is a polynucleotide described in the exemplification of
CC	the invention
SQ	
	Sequence 470 BP; 75 A; 103 C; 141 G; 151 T; 0 U; 0 Other;
	Query Match            63.7%; Score 289; DB 6; Length 470;
	Best Local Similarity   100.0%; Pred. No. 1.9e-129;
	Matches   289; Conservative   0; Mismatches   0; Indels   0; Gaps   0
OY	166 GGATCCTCGGGGGAATGGGGCTTCGGATGTAGATCTGATCCGCCGTGTTGGGGAGA 225
DB	166 GGATCCTCGGGGGAATGGGGCTTCGGATGTAGATCTGATCCGCCGTGTTGGGGAGA 225
OY	226 TGATGGGGCGTTAAATAATTCCCATGCATCTAACAAGATCAGAGAAGGGAAAAAGGGCAC 285
DB	226 TGATGGGGCGTTAAATAATTCCCATGCATCTAACAAGATCAGAGAAGGGAAAAAGGGCAC 285
OY	286 TATGTTTAAATTTTTTAATATTTCTGCTGCTGCTCTGTCAAGCTTGAGTGTCTAATCT 345
DB	286 TATGTTTAAATTTTTTAATATTTCTGCTGCTGCTCTGTCAAGCTTGAGTGTCTAATCT 345
OY	346 TTCTTTCTCTTTTGTGGGTGAATTTGAATCCACAGATTTGTCATCGTAGTTTTT 405
DB	346 TTCTTTCTCTTTTGTGGGTGAATTTGAATCCCTCAGCATTTGTCATCGTAGTTTTT 405
OY	406 CTTTTCATGATTTGTGACAAATGACAGCCTCGTGCAGAGCTTTTGTAG 454
DB	406 CTTTTCATGATTTGTGACAAATGACAGCCTCGTGCAGAGCTTTTGTAG 454
RESULT 9	
ADFA9181	
ID	ADFA9181 standard; DNA; 470 BP.
XX	
AC	ADFA9181;
XX	
DT	12-FEB-2004 (first entry)
XX	
DE	Rice actin intron.
XX	
KW	receptor cassette; chimeric receptor polypeptide; DNA binding domain;
KW	hinge domain; ecdysone receptor; ECR; ligand binding domain;
KW	activation domain; transgenic seed; transgenic plant; plant line;
KW	herbicide; pesticide; rice; actin; intron; de.
XX	
OS	Oryza sp.
XX	
PN	US2003154509-A1.

XX	PD	14-AUG-2003.
XX	PF	24-OCT-2001; 2001US-00087167.
XX	PR	24-OCT-2001; 2001US-00087167.
XX	PA	(PASC/) PASCAL E J.
XX	PA	(VALE/) VALENTINE S A.
XX	PA	(BROW/) BROWN J A.
XX	PA	(COCK/) COCKRELL A S.
XX	PI	(JOHN/) JOHNSON B D.
XX	DR	Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX	WT	WPI; 2003-897756/82.
XX	PT	New receptor cassette encoding a chimeric receptor polypeptide, useful
XX	PT	for regulating the expression of target polypeptides in plants in the
XX	PT	presence of appropriate chemical ligands.
XX	PS	Example 10; SEQ ID NO 109; 186pp; English.
XX	CC	The invention describes a receptor cassette encoding a chimeric receptor
XX	CC	polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
XX	CC	(D) domain of an eclysome receptor (ECR) of an insect, a ligand binding
XX	CC	(E) domain that is heterologous with respect to the D domain, and an
XX	CC	activation domain. The receptor cassette and method are useful in
XX	CC	regulating the expression of target polypeptides in plants in the
XX	CC	presence of appropriate chemical ligands. The transgenic seeds and plants
XX	CC	can be used for the breeding of improved plant lines that, for e.g.,
XX	CC	increase the effectiveness of conventional methods such as herbicide or
XX	CC	pesticide treatment. This sequence represents a rice actin intron used in
XX	CC	the construction of a monocot-expressible target expression cassette
XX	CC	comprising the firefly luciferase reporter gene and having response
XX	CC	elements for the GAL4 DNA binding domain.
XX	SQ	Sequence 470 BP, 75 A; 103 C; 141 G; 151 T; 0 U; 0 Other;
XX	Query Match	63.7%; Score 289; DB 10; Length 470;
XX	Best Local Similarity	100.0%; Pred. No. 1.9e-129;
XX	Matches 289; Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	Db	166 GGATTCCTGCGGGGAATGCGGCTCTCGGATGTAGATCTGCATCCGCCGTTGTTGGGGAGA 225
OY	Db	166 GGATTCCTGCGGGGAATGCGGCTCTCGGATGTAGATCTGCATCCGCCGTTGTTGGGGAGA 225
OY	Db	226 TGATGGGGCGTTTAAATTTCGGCATGCTAACAAGATCAGGAGAGGGGAAAAGGGCAC 285
OY	Db	226 TGATGGGGCGTTTAAATTTCGGCATGCTAACAAGATCAGGAGAGGGGAAAAGGGCAC 285
OY	Db	286 TAGGTATAATTTTTATATATTTCTGCTGCTCGTCAGGCTTAGATGTCTAGATCT 345
OY	Db	286 TAGGTATAATTTTTATATATTTCTGCTGCTCGTCAGGCTTAGATGTCTAGATCT 345
OY	Db	346 TTCTTTCTCTCTTTTGTTGGTAGAATTGGAATTCCTCAGCATTTGTCATCGGTAGTTT 405
OY	Db	346 TTCTTTCTCTCTTTTGTTGGTAGAATTGGAATTCCTCAGCATTTGTCATCGGTAGTTT 405
OY	Db	406 CTTTTCATGATTTTGTGACAAATGCAGCTCGTGGCGGACTTTTGTGTAG 454
OY	Db	406 CTTTTCATGATTTTGTGACAAATGCAGCTCGTGGCGGACTTTTGTGTAG 454
DE	RESULT 10	
DE	ID	ABZ70926
DE	ID	ABZ70926 standard; DNA; 1121 BP.
DE	XX	ABZ70926;
DE	XX	23-APR-2003 (first entry)
DE	XX	CyIIIA 3' fragment with the 3' end of rice actin 1 intron.

XX Transgenic organism; male sterility; herbicide resistance;  
 KW insecticide resistance; selectable marker; counter-selectable marker;  
 KM gene; ds.  
 XX Oryza sativa.  
 OS Synthetic.  
 PN WO200296192-A2.  
 PD 05-DEC-2002.  
 XX 29-APR-2002; 2002WO-EP004724.  
 PF 29-APR-2002; 2002WO-EP004724.  
 PR 29-APR-2002; 2002WO-EP004724.  
 XX (ICON-) ICON GENETICS AG.  
 PA (ICON-) ICON GENETICS AG.  
 PI Werner S, Marillonnet S, Klimyuk V, Gleba Y;  
 DR WPI; 2003-041365/03.  
 XX Producing a transgenic organism expressing a trait of interest where the  
 PT trait of interest is involved in male sterility.  
 PS Example 1; Page 25-26; 42pp; English.  
 XX The present invention describes a method for producing a transgenic  
 CC multicellular plant or animal organism expressing a trait of interest and  
 CC having a controlled distribution of the trait to progeny where the  
 CC process comprises hybridizing a first multicellular organism or a cell  
 CC thereof having a first heterologous DNA sequence comprising a first  
 CC fragment of a nucleotide sequence encoding said trait of interest and a  
 CC second multicellular organism or a cell thereof having a second  
 CC heterologous DNA sequence comprising a second fragment of the nucleotide  
 CC sequence encoding said trait of interest where each first and second  
 CC heterologous sequences are designed such that the trait of interest  
 CC arises due to RNA trans-splicing after said hybridisation. The method can  
 CC be used for producing a transgenic multicellular plant or animal organism  
 CC expressing a trait of interest where trait of interest is involved in  
 CC male sterility and is selected form herbicide resistance, insecticide  
 CC resistance, selectable marker, counter-selectable marker. The present  
 CC sequence represents a synthetic CryIIIA 3' fragment with the 3' end of  
 CC rice actin 1 intron, which is used in an example from the present  
 CC invention  
 CC  
 XX Sequence 1121 BP; 302 A; 284 C; 241 G; 294 T; 0 U; 0 Other;  
 SQ  
 Query Match 45.8%; Score 208; DB 10; Length 1121;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-90;  
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC ADP73931;  
 XX 09-SEP-2004 (first entry)  
 DT Plasmid pDA8505, SEQ ID NO:85, encoding mAb HX8 (both chains).  
 XX  
 DE Transgenic plant; immunoglobulin production; recombinant production;  
 KW glycosylation; fucose; glycan; virucide; immunotherapy; maize;  
 KW gamma-zeln promoter; rice; actin promoter;  
 KW phosphinothricin acyltransferase; PAT; mouse; leader sequence;  
 KW herpes simplex virus; HSV1; HSV2; human; monoclonal antibody HX8; IgA;  
 KW heavy chain; light chain; codon optimised; plasmid; pDA8505; cyclic;  
 KM circular; ds.  
 XX Zea mays.  
 OS Mus sp.  
 OS Homo sapiens.  
 OS Oryza sativa.  
 OS Chimeric.  
 OS Synthetic.  
 OS Unidentified.  
 XX  
 FH Key  
 FH misc\_feature  
 FT Location/Qualifiers  
 FT 424..1589  
 FT /tag= a  
 FT /label= SAR  
 FT /note= "scaffold attachment region. Also referred to as  
 FT MAR (matrix association region)"  
 FT 1673..3175  
 FT /tag= b  
 FT /note= "Maize gamma-zein promoter"  
 FT 3178..4671  
 FT /tag= d  
 FT /product= "heavy chain of human anti-HSV1/HSV2 monoclonal  
 FT IgA antibody HX8 (with mouse leader sequence)"  
 FT 3178..3234  
 FT /tag= c  
 FT /note= "mouse leader sequence"  
 FT 3235..4668  
 FT /tag= e  
 FT /product= "Mature HX8 heavy chain"  
 FT 4678..5045  
 FT /tag= f  
 FT /note= "Maize per5 3'UTR"  
 FT 5157..6659  
 FT /tag= g  
 FT /note= "Maize gamma-zein promoter"  
 FT 6662..7363  
 FT /tag= i  
 FT /product= "Heavy chain of human anti-HSV1/HSV2 monoclonal  
 FT IgA antibody HX8 (with mouse leader sequence)"  
 FT 6662..6718  
 FT /tag= h  
 FT /note= "mouse leader sequence"  
 FT 6719..7360  
 FT /tag= j  
 FT /product= "Mature HX8 heavy chain"  
 FT 7370..7737  
 FT /tag= k  
 FT /note= "Maize per5 3'UTR"  
 FT 7889..9258  
 FT /tag= l  
 FT /note= "Rice actin promoter/intron"  
 FT 9261..9815  
 FT /tag= m  
 FT /product= "phosphinothricin acyltransferase (PAT)"  
 FT /note= "the PAT coding region is given in the  
 FT specification as positions 9260-9820"  
 FT 9831..10162  
 FT /tag= n  
 FT /note= "Maize lipase 3'UTR"  
 FT 10229..11394  
 FT /tag= o  
 FT misc\_feature

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FT /label= SAR
FT /note= "Scaffold attachment region. Also referred to as
FT MAR (matrix association region)"
XX
XX
XX WO2004050838-A2.
XX
XX 17-JUN-2004.
XX
XX 28-NOV-2003; 2003WO-US037905.
XX
XX 27-NOV-2002; 2002US-0429385P.
XX
XX (DOMC ) DOM CHEM CO.
XX (DOMC ) DOM AGROSCIENCES LLC.
XX (EPIC-) EPICYTE PHARM INC.
XX
XX Briggs K, Glancy T, Hein MB, Hiatt AC, Karnoup AL, Anderson WHK,
XX Pareddy D, Petolino J, Rubin-Wilson B, Taylor D, Roberts JL,
XX
XX WPI; 2004-46111/43.
XX P-PSDB; ADP73848, ADP73856.
XX
XX Novel plant-produced immunoglobulin having glycopeptide or glycan profile
XX with reduced fucosylation, useful for treating herpes simplex virus
XX infection.
XX
XX Claim 69; SEQ ID NO 85; 212pp; English.
XX
XX The invention relates to the production of immunoglobulins in plants,
XX wherein at least a portion of the glycans attached to the immunoglobulins
XX lack fucose. The immunoglobulins produced can be of any class (i.e., IgG,
XX IgA, IgM, IgE or IgD) and is especially an anti-herpes simplex virus
XX (HSV) antibody or an anti-alphaherpes3, alphaherpes dual integrin
XX antibody. The invention also relates to constructs, plasmids and vectors
XX for producing the immunoglobulins; transformed plant cells, calli, plant
XX tissues and whole plants for producing the immunoglobulins; methods for
XX producing the immunoglobulins, the immunoglobulins thus produced; and the
XX use of such immunoglobulins. The immunoglobulins of the invention may be
XX used to treat HSV infection or tumour angiogenesis. The invention
XX provides the advantages of antibody production in plants, such as large
XX scale production, reduced costs, and elimination of pathogenic
XX contaminants such as viruses and prions, with a simplified (i.e., non-
XX plant-specific) glycosylation profile which reduces the risk that the
XX immunoglobulin may not be functional in animals. The present sequence
XX represents the plasmid pDA8505, which contains codon optimised DNA
XX sequences encoding the heavy and light chains of the human anti-HSV1/HSV2
XX monoclonal IgA antibody H8 each of which are fused to mouse leader
XX sequences. Both heavy and light chain fusion genes are under the control
XX of maize endosperm-specific gamma-zein promoters. The plasmid also
XX contains a phosphinothricin acyltransferase (PAT) gene under the control
XX of a rice actin promoter.
XX
XX Sequence 13680 BP; 3886 A; 3069 C; 2934 G; 3788 T; 0 U; 3 Other;
SQ
Query Match 44.9%; Score 204; DB 12; Length 13680;
Best Local Similarity 100.0%; Pred. No. 2.6e-88;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTAAACACCCCGCCCTCTCTCTTCTTCTTCGCTTTTCTTCTTCGCTCTCGAT 60
DB 8796 GTAAACACCCCGCCCTCTCTCTTCTTCTTCGCTTTTCTTCTTCGCTCTCGAT 8855
QY 61 CTTTGACCTTGATGTTGGGTGGGAGAGAGCGGCTTGTGCGCCAGATGGTGGCGGG 120
DB 8856 CTTTGACCTTGATGTTGGGTGGGAGAGAGCGGCTTGTGCGCCAGATGGTGGCGGG 8915
QY 121 AGGAGCGGAGATCTCGCGGCTGCGCTCTCGGAGCGTGAAGTGGCCCGGATCTCGCGGGGA 180
DB 8916 AGGAGCGGAGATCTCGCGGCTGCGCGCTCTCGGAGCGTGAAGTGGCCCGGATCTCGCGGGGA 8975
QY 181 ATGGGCTCTCGAGTGAATCTG 204
DB 8976 ATGGGCTCTCGAGTGAATCTG 8999
```

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RESULT 12
ID ADG69912
XX ADG69912 standard; DNA; 1259 BP.
XX
XX ADG69912;
XX
XX 11-MAR-2004 (first entry)
XX
XX Actin promoter and nucleotide sequence.
XX
XX transgenic plant; ferulic acid esterase; FAE; enzyme; phenolic acid;
XX plant; cell wall; improved digestibility; biomass conversion;
XX highly fermentable carbohydrate; gene; dg.
XX
XX Synthetic.
XX
XX WO200268666-A1.
XX
XX 06-SEP-2002.
XX
XX 16-NOV-2001; 2001WO-US043586.
XX
XX 17-NOV-2000; 2000US-0249608P.
XX
XX (GENEV ) GENENCOR INT INC.
XX
XX Dunn-Coleman N, Langdon T, Morris P;
XX
XX WPI; 2002-698675/75.
XX
XX New transgenic plant comprising an expression cassette with a promoter
XX operably linked to a ferulic acid esterase encoding polynucleotide,
XX useful in improving digestibility for livestock and enhancing biomass
XX conversion.
XX
XX Disclosure; Fig 50A-B; 208pp; English.
XX
XX The present invention describes a transgenic plant (I) comprising an
XX expression cassette with a promoter operably linked to a ferulic acid
XX esterase encoding polynucleotide. Also described: (1) controlling (M1)
XX the level of phenolic acids in plant cell walls of a transgenic plant by
XX introducing into the plant an expression cassette comprising a promoter
XX operably linked to a ferulic acid esterase encoding polynucleotide; and
XX (2) a transgenic plant (II) produced by (M1). The transgenic plants are
XX useful in improving digestibility for livestock and enhancing biomass
XX conversion. The method is useful for enhancing the production of more
XX highly fermentable carbohydrates in plants, especially forage grasses.
XX The expression cassette is useful for controlling the level of phenolic
XX acids in plant cell walls of a transgenic plant. The present sequence is
XX used in the exemplification of the present invention.
XX
XX Sequence 1259 BP; 337 A; 332 C; 268 G; 322 T; 0 U; 0 Other;
SQ
Query Match 44.7%; Score 203; DB 6; Length 1259;
Best Local Similarity 100.0%; Pred. No. 7.7e-88;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTAAACACCCCGCCCTCTCTCTTCTTCTTCGCTTTTCTTCTTCGCTCTCGAT 60
DB 929 GTAAACACCCCGCCCTCTCTCTTCTTCTTCGCTTTTCTTCTTCGCTCTCGAT 988
QY 61 CTTTGACCTTGATGTTGGGTGGGAGAGAGCGGCTTGTGCGCCAGATCGGTGGCGGG 120
DB 989 CTTTGACCTTGATGTTGGGTGGGAGAGAGCGGCTTGTGCGCCAGATCGGTGGCGGG 1048
QY 121 AGGAGCGGAGATCTCGCGGCTGCGCTCTCGGAGCGTGAAGTGGCCCGGATCTCGCGGGGA 180
DB 1049 AGGAGCGGAGATCTCGCGGCTGCGCGCTCTCGGAGCGTGAAGTGGCCCGGATCTCGCGGGGA 1108
QY 181 ATGGGCTCTCGAGTGAATCT 203
DB 1108 ATGGGCTCTCGAGTGAATCT 203
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OW nucleic - nucleic search, using sw model

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EST:\*  
1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hlc.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gss1.\*  
9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72	15.9	542	5	BQ609717 BRY_5803
2	25	5.5	991	9	CL076535 CH216-139
3	24	5.3	1205	9	AG380362 Mus muscu
4	22	4.8	662	7	CL343092 RPL144.27
5	22	4.8	687	9	AG121527 Pan trogl
6	22	4.8	997	6	CB561980 AGENCOURT
7	21	4.6	123	9	BX232968 Danio rer
8	21	4.6	430	9	CG198335 PUFMC48TB
9	21	4.6	453	2	BF558554 UI-R-E0-d
10	21	4.6	505	7	CF740605 UI-M-HC0-
11	21	4.6	555	8	AG631272 RPL1-11-4
12	21	4.6	604	8	BH558342 BOG1A74TR
13	21	4.6	654	7	CF828591 UCRCR01_0
14	21	4.6	655	7	CO746318 tah89a09.
15	21	4.6	657	7	CF828592 UCRCR01_0
16	21	4.6	743	1	AL693283 AL693283
17	21	4.6	767	7	BX986759 Forward s
18	21	4.6	793	9	AG525416 Mus muscu
19	21	4.6	807	8	B20652 B20652
20	21	4.6	828	9	CG876902 HSC 00941
21	21	4.6	894	6	CL475111 SAIL 231
22	21	4.6	927	5	BX455358 BX455358
23	21	4.6	1071	9	CL103786 ISB1-41P2
24	21	4.6	1077	4	BG105171 BG105171

25	21	4.6	1195	9	AG393152 Mus muscu
26	21	4.6	1224	9	AG524895 Mus muscu
27	21	4.6	1345	8	CC238075 CH261-132
28	21	4.6	1712	4	BG760522 602716959
29	20	4.4	139	2	BE138943 xtc63d05.x
30	20	4.4	188	1	AI355517 qt96d12.x
31	20	4.4	214	2	BB524812 BB524812
32	20	4.4	222	2	BE857906 BE857906
33	20	4.4	227	1	AI273903 AI273903
34	20	4.4	235	7	CN38434 CN38434
35	20	4.4	243	4	BM829427 K-EST0102
36	20	4.4	245	8	AZ353546 AZ353546
37	20	4.4	253	4	B1068455 C022P21U
38	20	4.4	254	4	BF959480 QV4-FT000
39	20	4.4	265	1	AV312223 AV312223
40	20	4.4	268	2	AW948856 QV4-FT000
41	20	4.4	271	4	BG073230 H3120C03-
42	20	4.4	271	5	BU674968 UI-CF-DU0
43	20	4.4	276	1	AI749380 at23c03.x
44	20	4.4	277	2	BB301206 BB301206
45	20	4.4	280	2	BB080651 BB080651

#### ALIGNMENTS

RESULT 1  
BQ609717 542 bp mRNA linear EST 25-JUN-2002  
LOCUS BRY\_5803 wheat EST endosperm library Triticum aestivum cDNA 5',  
DEFINITION mRN sequence.  
ACCESSION BQ609717 GI:21559056  
VERSION BQ609717.1  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
1 (bases 1 to 542)  
REFERENCE Clarke,B., Lambrecht,M. and Rhee,S.Y.  
Arabidopsis genomic information for interpreting wheat EST  
sequences  
JOURNAL Funct. Integr. Genomics 3 (1-2), 33-38 (2003)  
MEDLINE 22478026  
PUBMED 12590341

COMMENT  
Contact: Lambrecht M  
The Arabidopsis Information Resource  
Carnegie Institution of Washington, Dept. of Plant Biology  
260 Panama Street, Stanford, CA 94305, USA  
Tel: 1 650 325 1521 x 251  
Fax: 1 650 325 3748  
Email: rhee@coms.stanford.edu.  
location/Qualifiers  
1. .542  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultivar="WYuna"  
/db\_xref="taxon:4565"  
/tissue\_type="endosperm"  
/dev\_stage="developing endosperm tissue 8, 10 and 12 DPA  
(days post anthesis)"  
/clone\_lib="wheat EST endosperm library"

#### FEATURES

source

#### ORIGIN

Query Match 15.9% Score 72; DB 5; Length 542;  
Best Local Similarity 100.0%; Pred. No. 2.9e-26;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CGCATGCTTAACAGATCAGAAAGGCGGCACTATGTTATATTTTATAT 305  
DB 148 CGCATGCTTAACAGATCAGAAAGGCGGCACTATGTTATATTTTATAT 207



QY 306 ATTCTGCTGCT 317  
 |||||  
 Db 208 ATTCTGCTGCT 219

RESULT 2  
 CL076535  
 LOCUS  
 DEFINITION CH216-139N11 991 bp DNA linear GSS 31-DEC-2003  
 CH216-139N11, genomic survey sequence.

ACCESSION CL076535  
 VERSION CL076535  
 KEYWORDS GSS.  
 SOURCE Xenopus tropicalis (western clawed frog)  
 ORGANISM Xenopus tropicalis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 Xenopodinae; Xenopus; Silurana.  
 1 (bases 1 to 991)  
 Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,  
 Wardis, E., and Wilson, R.  
 A physical map of the xenopus tropicalis genome  
 Unpublished (2003)  
 Contact: Richard K Wilson  
 Genome Sequencing Center  
 Washington University School of Medicine  
 Email: submissions@wustl.edu  
 Insert Length: 175000 Std Error: 0.00  
 Seq primer: RML TACGACTCACTAAGCGAGA  
 Class: BAC ends  
 High quality sequence start: 11  
 High quality sequence stop: 99.  
 Location/Qualifiers  
 1..991  
 /organism="Xenopus tropicalis"  
 /mol\_type="genomic DNA"  
 /strain="Nigerian frog"  
 /db\_xref="taxon:8364"  
 /clone="CH216-139N11"  
 /sex="male"  
 /cell\_line="Stock 248 F7A2, Inbred N7"  
 /clone\_1lb="CH216"  
 /note="Vector: PTARBA2.1; CHORI-216 Xenopus tropicalis  
 BAC library"

ORIGIN

Query Match 5.5%; Score 25; DB 9; Length 991;  
 Best Local Similarity 100.0%; Pred. No. 0.13;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCCCGCCCTCTCTCTTTCTT 29  
 |||||  
 Db 680 CCACCCCGCCCTCTCTCTTTCTT 704

RESULT 3  
 AG380362/c 1205 bp DNA linear GSS 03-JUN-2004  
 LOCUS Mus musculus molossinus DNA, clone:MSMG01-189W20.T7, genomic survey  
 sequence.  
 AG380362  
 ACCESSION AG380362.1 GI:47991567  
 VERSION GSS.  
 KEYWORDS Mus musculus molossinus  
 SOURCE Mus musculus molossinus  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.  
 BAC end Sequences of Library MSMG01  
 1 (bases 1 to 1205)  
 Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS

TITLE Direct Submission  
 JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan  
 1-7-22 Suenho-chou, Tsukuba, Ibaraki, Japan  
 (E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,  
 Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
 Clones are derived from the mouse BAC library MSMG01. For BAC  
 library availability, please contact Kuniya Abe (abe@rtc.riken.jp).  
 Tsukuba Institute, Bio Resource Center,  
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1  
 Koyadai, Tsukuba, 305-0074 Japan  
 phone: 81-298-36-9189, fax: 81-298-36-9199  
 e-mail: abe@rtc.riken.jp

COMMENT  
 PRIMERS  
 Sequencing : T7  
 LIBRARY : pBAC3.6  
 Vector :  
 R.Site 1 : EcoRI  
 R.Site 2 : EcoRI.  
 Location/Qualifiers  
 1..1205  
 /organism="Mus musculus molossinus"  
 /mol\_type="genomic DNA"  
 /sub\_species="molossinus"  
 /db\_xref="taxon:57486"  
 /clone="MSMG01-189W20.T7"  
 /sex="male"  
 /issue\_type="mixture of kidney and spleen"  
 /clone\_1lb="MSMG01 Mouse Male BAC library"

ORIGIN

Query Match 5.3%; Score 24; DB 9; Length 1205;  
 Best Local Similarity 100.0%; Pred. No. 0.43;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTTTCTTCTCCGTTTTTTTTTC 46  
 |||||  
 Db 379 CTTTCTTCTCCGTTTTTTTTTTC 356

RESULT 4  
 CL343092 662 bp DNA linear GSS 19-AUG-2004  
 LOCUS RPCI44.276C24.f RPCI-44 Sus scrofa genomic clone RPCI44\_276C24,  
 genomic survey sequence.  
 CL343092  
 ACCESSION CL343092.1 GI:51395060  
 VERSION GSS.  
 KEYWORDS Sus scrofa (pig)  
 SOURCE Sus scrofa  
 ORGANISM Sus scrofa  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.  
 Rogatcheva, M.B., Meyers, S., He, W., Larkin, D.M., Marron, B.M.,  
 Beever, J.E. and Schook, L.B.  
 Piggy-BACing the Human Genome: Constructing a Porcine Physical Map  
 Through Comparative Genomics  
 Unpublished (2004)  
 Other GSSs: RPCI44\_276C24.r  
 Contact: Lawrence B. Schook  
 Department of Animal Sciences  
 University of Illinois at Urbana Champaign  
 1201 W. Gregory Dr., Urbana, IL 61801, USA  
 Tel: 217 265 5326  
 Fax: 217 244 5617  
 Email: schook@uiuc.edu  
 Clones are derived from the porcine BAC library RPCI-44  
 (http://www.bacpac.chori.org/porcine242.htm). For BAC library  
 availability, please contact Pieter de Jong (pdjong@chori.org).  
 Clones may be purchased from BACpac Resources  
 (http://BACpacResources.chori.org). This work was undertaken as part  
 of the International Swine Genome Sequencing Consortium by  
 University of Illinois at Urbana Champaign, USA with funds provided

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS

by grant No. AG2002-34480-11828 from USDA-CSREES and  
AG2001-35205-09965 from USDA/NRI (Livestock Genome Sequencing  
Initiative)  
Plate: 276 row: C column: 24  
Seq primer: T7  
Class: BAC ends.

# FEATURES

## source

Location/Qualifiers  
1..662  
/organism="Sus scrofa"  
/mol\_type="genomic DNA"  
/strain="four pigs (breed: 37.5% Yorks Landrace and 25%  
Meishan)"  
/db\_xref="taxon:9823"  
/clone="RPC144\_276C24"  
/sex="male"  
/cell\_type="Dlood"  
/clone\_id="RPC1-44"  
/note="Vector: pFARBAC2; Site 1: ECORI; Site 2: BORI;  
porcine male BAC library produced by Pieter de Jong"

## ORIGIN

Query Match 4.8%; Score 22; DB 9; Length 662;  
Best Local Similarity 100.0%; Pred. No. 4.9;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 339 TAGATCTTCTTCTTCTTCTT 360  
|||||  
2 TAGATCTTCTTCTTCTTCTT 23

## Db

RESULT 5  
AG121527 687 bp DNA linear GSS 04-NOV-2001  
LOCUS Pan troglodytes DNA, clone: PTB-130J16.F, genomic survey sequence.  
DEFINITION AG121527  
ACCESSION AG121527.1 GI:16650692  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Pan troglodytes (Chimpanzee)  
Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

# REFERENCE

1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,  
Toto, Y., Watanabe, H. and Sakaki, Y.  
BAC end sequences of library PTB

Unpublished

2 (bases 1 to 687)

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,  
Toto, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Submitted (02-AUG-2001) Aaso Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail: chimpanzee@sc.riken.go.jp, URL: http://hsp.gsc.riken.go.jp/  
Tel: 81-45-503-9111, Fax: 81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB. This BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.

PRIMERS

Sequencing: -21M13  
LIBRARY

Vector : PKS145  
R.Site 1 : SacI  
R.Site 2 : SacI.

Location/Qualifiers

1..687  
/organism="Pan troglodytes"

/mol\_type="genomic DNA"

/db\_xref="taxon:9598"

/clone="PTB-130J16.F"

/sex="male"

/cell\_type="lymphoblast"

/clone\_id="PTB Chimpanzee Male BAC Library"

## ORIGIN

Query Match 4.8%; Score 22; DB 9; Length 687;  
Best Local Similarity 100.0%; Pred. No. 4.9;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCCTCTCTTCTTCTTCTTCC 34  
|||||  
638 CCCCTCTCTTCTTCTTCTC 659

## Db

RESULT 6  
CB561980 997 bp mRNA linear EST 02-APR-2003  
LOCUS AGENCOURT\_13324979 NICHHD\_XGC\_Tad1 Xenopus laevis cDNA clone  
DEFINITION IMAGE:6880820 3', mRNA sequence.  
CB561980  
ACCESSION CB561980.1 GI:29481510  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Xenopus laevis (African clawed frog)  
Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
Xenopodinae; Xenopus; Xenopus.

## REFERENCE

1 (bases 1 to 997)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncigap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Drs. Donald Brown and Liqun Cai  
CDNA Library Preparation: CLONTECH  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LILNL at:  
http://image.llnl.gov  
Plate: LILNL3124 row: n column: 19  
High quality sequence start: 4  
High quality sequence stop: 231.

## FEATURES

## source

Location/Qualifiers  
1..997  
/organism="Xenopus laevis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8355"  
/clone="IMAGE:6880820"  
/dev\_stage="metamorphosis stage 53"  
/clone\_id="NICHHD\_XGC\_Tad1"  
/note="Organ: Developing Tadpole; Vector: pDNR-LIB;  
Site 1: Sfi; Site 2: Sfi; 5' and 3' adaptors were used in  
cloning as follows: 5' adaptor sequence:  
5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCCAGCGCGCCACATG-dT(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.6 kb  
(range 0.9-3.0 kb). 15/15 colonies contained inserts by  
PCR. This library was enriched for full-length clones and  
was constructed by Clontech Laboratories (Palo Alto, CA)."

## ORIGIN

Query Match 4.8%; Score 22; DB 6; Length 997;  
Best Local Similarity 100.0%; Pred. No. 4.9;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY

18 CTCCTCTTCTTCTTCTCGTTT 39  
|||||  
762 CTCCTCTTCTTCTTCTCGTTT 741

## Db

RESULT 7  
BX232968 123 bp DNA linear GSS 13-MAR-2003  
LOCUS BX232968/c  
DEFINITION Danio rerio genomic clone DKRY-282L1, genomic survey sequence.

```

ACCESSION   BX232968
VERSION     BX232968.1  GI:28067118
KEYWORDS
SOURCE      Danio rerio (zebrafish)
ORGANISM    Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
            1 (bases 1 to 123)
REFERENCE   1 (bases 1 to 123)
AUTHORS     Humphray, S.J., Huckle, E. and Durham, J.L.
TITLE       Direct Submision
JOURNAL     Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humphray@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the T7 end of BAC 282L1. 282L1 is
            part of the Daniokey BAC library created by R. Plaetzer and N.V.
            Keygene. Further details:
            http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES
source      1..123
            /organism="Danio rerio"
            /mol_type="genomic DNA"
            /db_xref="taxon:7955"
            /clone="DKEY-282L1"
            /issue_type="Testis"
            /note="Vector pindigobAC-536"

ORIGIN
Query Match      4.6%; Score 21; DB 9; Length 123;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      292 TTATTTTATATATTTCTG 312
         |||||
Db       75 TTATTTTATATATTTCTG 55

RESULT 8
LOCUS     CG198335 430 bp DNA linear GSS 21-AUG-2003
DEFINITION PUFMC48TB_ZM_0.6_1.0_KB Zee may's genomic clone ZMMBTa0681H23,
            genomic survey sequence.
ACCESSION CG198335
VERSION   CG198335.1 GI:34089396
KEYWORDS  GSS.
SOURCE    Zee may's
            Zee may's
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
            1 (bases 1 to 430)
REFERENCE   1 (bases 1 to 430)
AUTHORS     Whiteley, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
            Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
            Bennettzen, J.
TITLE       Maize Genomics Consortium
JOURNAL     Unpublished (2003)
COMMENT     Other_GSSs: PUFMC48TD
            Contact: Cathy Whiteley
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whiteley@tigr.org
            Seq primer: TR
            Class: sheared ends.
FEATURES
source      1..430
            /organism="Zea may's"
            /mol_type="genomic DNA"
            /strain="B73"
            /db_xref="taxon:4577"
            /clone="ZMMBTa0681H23"
            /clone_1tb="ZM_0.6_1.0_KB"

```

```

/Note="Vector: PCR4-TOPO, Site_1: EcoRI, 0.6-1.0 kb high
COT selected genomic DNA library"

ORIGIN
Query Match      4.6%; Score 21; DB 9; Length 430;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      343 TCTTCTTCTCTTTTGTG 363
         |||||
Db       172 TCTTCTTCTCTTTTGTG 152

RESULT 9
LOCUS     BF558554 453 bp mRNA linear EST 12-DEC-2000
DEFINITION UI-R-E0-dg-f-11-0-UI.r1 UI-R-E0 Rattus norvegicus cDNA clone
            BF558554
            UI-R-E0-dg-f-11-0-UI 5', mRNA sequence.
ACCESSION   BF558554
VERSION     BF558554.1 GI:11668284
KEYWORDS
SOURCE      Rattus norvegicus (Norway rat)
            Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
            1 (bases 1 to 453)
REFERENCE   1 (bases 1 to 453)
AUTHORS     Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE       Normalization and subtraction: two approaches to facilitate gene
            discovery
JOURNAL     Genome Res. 6 (9), 791-806 (1996)
MEDLINE    97044477
PUBMED     8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@iowa.edu
            cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            clones will be available through Research Genetics (www.regen.com)
            This clone is also available through the I.M.A.G.E. Consortium at
            LBNL (info@image.llnl.gov). IMAGE ID=177947 The following
            repetitive elements were found in this cDNA sequence: 14-73,
            >POLY_A#Simple_repeat 91-239, >B1_MM#SINE/Alu 293-414,
            >(GAA)n#Simple_repeat
            Seq primer: M13 Forward.
            Location/Qualifiers
            1..453
            /organism="Rattus norvegicus"
            /mol_type="mRNA"
            /strain="Sprague-Dawley"
            /db_xref="taxon:10116"
            /clone="UI-R-E0-dg-f-11-0-UI"
            /dev_stage="embryonic"
            /lab_host="DH10B (Life Technologies)"
            /clone_1tb="UI-R-E0"
            /note="Vector: pTRT3D-Pac (Pharmacia) with a modified
            polylinker; Site_1: NotI; Site_2: EcoRI; This library
            consists of a mixture of individually tagged normalized
            libraries constructed from 8, 12 and 18-day embryo. The
            tag is a string of 3-5 nucleotides present between the
            Not I site and the oligo-dT track which allows
            identification of the library of origin of a clone within
            the mixture."

ORIGIN
Query Match      4.6%; Score 21; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      343 TCTTCTTCTCTTTTGTG 363

```

Db 302 TCTTTCTCTCTCTTTGTC 282

## RESULT 10

CF740605 505 bp mRNA linear EST 10-OCT-2003  
LOCUS CF740605/c  
DEFINITION UI-M-HCO-CKY-j-06-0-UI.r1 NIH-BMAP\_HCO Mus musculus cDNA clone

IMAGE:30609533 5', mRNA sequence.

## ACCESSION

CF740605

## VERSION

CF740605.1

## KEYWORDS

EST.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 505)

## AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

## TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

## JOURNAL

Unpublished (1999)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: [cgapds-remail.nih.gov](mailto:cgapds-remail.nih.gov)  
Tissue Procurement: Dr. James Ian University of Iowa  
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clome Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/mousefl.html>  
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

The following repetitive elements were found in this cDNA  
sequence: 375-414, >(CAAA)n#Simple\_repeat (matched complement)  
Seq primer: pYX-5.

## FEATURES

Location/Qualifiers

1..505  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:30609533"  
/tissue\_type="whole eye"  
/dev\_stage="embryo 12.5,13.5,14.5 dpc"  
/lab\_host="DH10B (T1 phage resistant)"  
/clone\_1lb="NIH\_BMAP\_HCO"  
/note="Organ: Eye; Vector: pYX-Asc; Site 1: EcoRI I;  
Site 2: Not I; The library was constructed according  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured RNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with oligo-dT  
primer containing a Not I site. Double strand cDNA was  
size selected according to mRNA size fraction, ligated  
with EcoRI adaptor, digested with NotI and then cloned  
directionally into pYX-Asc vector. The library tag  
sequence located between the Not I site and the polyA tail  
is TTAATGAAGT. This library was created for the University  
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
Developing Mouse Nervous System', supported by National  
Institute of Mental Health (NIMH)."

## ORIGIN

Query Match 4.6%; Score 21; DB 7; Length 505;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 340 AGATCTTCTCTCTCTTTT 360

Db 38 AGATCTTCTCTCTCTTTT 18

## RESULT 11

AO631272/c

LOCUS

DEFINITION

AO631272 555 bp DNA linear GSS 17-JUN-1999  
RPT-11-482H7.TV RPT-11 Homo sapiens genomic clone RPT-11-482H7,

genomic survey sequence.

## ACCESSION

AO631272

## VERSION

AO631272.1

## KEYWORDS

GSS.

## SOURCE

Homo sapiens

## ORGANISM

Homo sapiens (human)

## REFERENCE

1 (bases 1 to 555)

## AUTHORS

Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and  
Venter,J.C.

## TITLE

Use of BAC End Sequences from Library RPT-11 for Sequence-Ready  
Map Building (1997)

## JOURNAL

Unpublished (1997)

## COMMENT

Contact: Shaying Zhao, William Nierman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: [hbeetlgr.org](mailto:hbeetlgr.org)  
Clones are derived from the human BAC library RPT-11. For BAC  
library availability, please contact Pieter de Jong  
([pieterdejong.med.bufileo.edu](mailto:pieterdejong.med.bufileo.edu)). Clones may be purchased from  
BACPAC Resources (<http://bacpac.med.bufileo.edu/ordering>) or from  
Research Genet cs ([info@resgen.com](mailto:info@resgen.com)). BAC end search page:  
[http://www.tigr.org/tdb/hungen/bac\\_end\\_search.html](http://www.tigr.org/tdb/hungen/bac_end_search.html).  
Seq primer: T7  
Class: BAC ends.

## FEATURES

Location/Qualifiers

1..555  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="GDB:7684878"  
/db\_xref="taxon:9606"  
/clone="RPT-11-482H7"  
/sex="Male"  
/cell\_type="Lymphocytes"  
/clone\_1lb="RPT-11"  
/note="Vector: pBAC3.6; Site 1: EcoRI, Site 2: EcoRI;  
RC111 Human Male BAC Library"

## ORIGIN

Query Match 4.6%; Score 21; DB 8; Length 555;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 340 AGATCTTCTCTCTCTTTT 360

Db 333 AGATCTTCTCTCTCTTTT 313

## RESULT 12

BH558342/c

LOCUS

DEFINITION

BOGIA74TR BOGI Brassica oleracea genomic clone BOGIA74, genomic  
survey sequence.

## ACCESSION

BH558342

## VERSION

BH558342.1

## KEYWORDS

GSS.

## SOURCE

Brassica oleracea

## ORGANISM

Brassica oleracea

## REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

## AUTHORS

1 (bases 1 to 604)

## TITLE

Whole genome shotgun sequencing of Brassica oleracea

## JOURNAL

Unpublished (2001)

## COMMENT

Other GSSs: BOGIA74TF  
Contact: Chris Town  
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtowne@igf.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TR  
 Class: sheared ends.

# FEATURES

Location/Qualifiers  
 1..604  
 /organism="Brassica oleracea"  
 /mol\_type="genomic DNA"  
 /strain="TO1000DH3"  
 /db\_xref="taxon:3712"  
 /clone="BOGIA74"  
 /note="Vector: PHOS1; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers"

## ORIGIN

Query Match 4.6%; Score 21; DB 8; Length 604;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 291 TTTATATTTTATATATTTCT 311  
 |||||  
 Db 305 TTTATATTTTATATATTTCT 285

## ORIGIN

Query Match 4.6%; Score 21; DB 7; Length 654;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 350 TTCTTCTTTTGTGGTAGAA 370  
 |||||  
 Db 562 TTCTTCTTTTGTGGTAGAA 582

1ab) collected twenty fruit in November 2002 and with assistance from Mu (Roose lab) pulled off pieces of peel, and then cut the inner 2 mm of albedo that was adjacent to the fruit and snap froze this material in liquid nitrogen. The fruit were beginning to turn orange but were still mostly green and were moderately easy to peel, with some easier than others. Frozen tissues were stored at -80C until further processing. Fenton (Close lab) purified RNA by the phenol method described in J. Japanese Soc. Hort. Sci. 1996. 64 (4): 809-814, purified poly(A) mRNA using a polyATrack mRNA Isolation System IV (Promega), produced a primary cDNA library using a lambda ZAP XR cDNA Synthesis Kit (Stratagene), then mass-excised one million plu from the primary library to produce a phagemid population. Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3730 at the Arizona Genomics Institute, University of Arizona (Kim, Kudrna, Wang, Yu). Chromatogram files were downloaded by FTP to UC Riverside (by Close), then processed at UC Riverside (by Wanmaker, Close lab) using the HarveST pipeline (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."

RESULT 13  
 CF828591 654 bp mRNA linear EST 29-OCT-2003  
 LOCUS UCRCR01.01N03 f Clementine Mandarin Albedo at Rind Separation cDNA  
 DEFINITION library Citrus reticulata cDNA clone CR\_CEA01N03, mRNA sequence.  
 ACCESSION CF828591  
 VERSION CF828591.1 GI:38026291  
 KEYWORDS EST.  
 SOURCE Citrus reticulata  
 ORGANISM Citrus reticulata  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Sapindales; Rutaceae; Citrus.  
 1 (bases 1 to 654)  
 Close,T.J., Roose,M.L., Federici,C.F., Mu,L., Fenton,R.D.,  
 Wanmaker,S., Kahn,T., Williams,T., Lovatt,C., Kim,H.R., Kudrna,D.,  
 Wang,R. and Yu,Y.  
 Development of EST Resources and New Genetic Markers for California  
 Citrus Clementine Mandarin Albedo at Rind Separation  
 Unpublished (2003)  
 CONTACT: Timothy Close  
 Department of Botany & Plant Sciences, University of California  
 Riverside, CA, 92521-0124  
 Tel: 9097873318  
 Fax: 9097874437  
 Email: timothy.close@ucr.edu  
 Seq primer: T7.  
 Location/Qualifiers  
 1..654  
 /organism="Citrus reticulata"  
 /mol\_type="mRNA"  
 /cultivar="Clementina Fina Sodea"  
 /db\_xref="taxon:85571"  
 /clone="CR\_CEA01N03"  
 /tissue\_type="Albedo"  
 /dev\_stage="12 year old trees"  
 /lab\_host="E. coli TUC121"  
 /clone\_lib="Clementine Mandarin Albedo at Rind Separation  
 cDNA Library"  
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid;  
 Site 1: EcoRI; Site 2: XhoI; Rind separation is a  
 prominent trait in Clementines. Kahn and Williams (UC  
 Riverside) advised that the best Clementine for this trait  
 is Fina Sodea. Lovatt (UC Riverside) provided advice on  
 which portion of the peel would be most likely to contain  
 transcripts related to rind separation. Federici (Roose

RESULT 14  
 CO746318/c 655 bp mRNA linear EST 30-JUL-2004  
 LOCUS tah89a09.y1 Hydra EST UCI 5 Hydra magnipapillata cDNA 5' similar to  
 DEFINITION SW:CLH1\_HUMAN Q00610 CLATHRIN HEAVY CHAIN 1 ;, mRNA sequence.  
 ACCESSION CO746318  
 VERSION CO746318.1 GI:50861127  
 KEYWORDS EST.  
 SOURCE Hydra magnipapillata  
 ORGANISM Hydra magnipapillata  
 Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;  
 Hydridae; Hydra.  
 1 (bases 1 to 655)  
 Bode,H., Blumberg,B., Steele,R., Wigge,P., Gee,L., Nguyen,Q.,  
 Martinez,D., Kibler,D., Hampson,S., Clifton,S., Pape,D., Marra,M.,  
 Hillier,L., Martin,J., Wylie,T., Dame,M., Theising,B., Bowers,Y.,  
 Gibbons,M., Ritter,E., Bennett,J., Ronko,I., Tsagarisvilli,R.,  
 Maguire,L., Kennedy,S., Waterson,R. and Wilson,R.  
 WashU Hydra EST Project  
 Unpublished (2002)  
 CONTACT: Hans Bode  
 WashU Hydra EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.edu  
 Library was constructed by Dick Lindgens, Univ. of Calif. Irvine  
 library materials provided by Hans Bode & Dick Lindgens, Univ. of  
 Calif. Irvine DNA sequencing by: Washington University Genome  
 Sequencing Center for information on obtaining a clone please  
 contact: Hans Bode (hrobde@uci.edu)  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 470.  
 Location/Qualifiers  
 1..655  
 /organism="Hydra magnipapillata"

```

/mol type="mRNA"
/strain="105"
/db_xref="taxon:6085"
/lab_host="DH10B"
/clone_1lb="Hydra EST UCI 5"
/notes="Vector: pSPORT1, Site 1: Not I; Site 2: Sal I;
a.1st strand cDNA was primed with a Not I primer-adaptor
(5' - pGACTAGTCTGATCGGACCGCCGCTT)15-3')
b.Double-stranded cDNA was ligated to Sal I adaptor,
digested with Not I and Sal I. c.The ligation mix was
pre-cut with Not I and Sal I. d.The cells were grown in
SOC = 5g yeast, 20g tryptone, 0.5g NaCl, 10 mM MgSO4, 10
mM MgCl, 0.2% glucose/liter, (no antibiotic). e.DMSO was
added to a final conc. of 10% as a cryoprotectant and
frozen f.The titre before freezing was determined as
~2400/100 ul. Assuming a 10% loss upon freezing, the titre
is probably ~2100/100 ul. g.9 tubes each containing ~
2100 clones/100 ul. h.Total of ~19,000 are enclosed.
h.The frequency of vectors containing inserts is 96% as
determined by digestion check after picking 24 clones,
mini-prep and subsequent digestion with Not I and Sal I.
i.A low level of 32p was used in the cDNA synthesis
procedure. The level measured by holding a Geiger Counter
next to a tube was background."

```

## ORIGIN

## Query Match

```

Best Local Similarity 100.0%; Pred.No.16;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 293 TATATTATTATATTTCTGC 313
Db 549 TATATTATTATATTTCTGC 529

```

```

4.6%; Score 21; DB 7; Length 655;

```

## ORIGIN

## Query Match

```

Best Local Similarity 100.0%; Pred.No.16;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 350 TTCTCTTTTGGGTAGAA 370
Db 93 TTCTCTTTTGGGTAGAA 73

```

```

Search completed: September 12, 2005, 14:04:06
Job time : 1937.56 secs

```

```

/clone_1lb="Clementine Mandarin Albado at Rind Separation
cDNA Library"
/notes="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: SmaI; Site 2: XhoI; Rind separation is a
prominent trait in Clementines. Kahn and Williams (UC
Riverside) advised that the best Clementine for this trait
is Fina Sodea. Lovatt (UC Riverside) provided advice on
which portion of the peel would be most likely to contain
transcripts related to rind separation. Federici (Roose
lab) collected twenty fruit in November 2002 and with
assistance from Mu (Roose lab) pulled off pieces of peel,
and then cut the inner 2 mm of albedo that was adjacent to
the fruit and snap froze this material in liquid nitrogen.
The fruit were beginning to turn orange but were still
mostly green and were moderately easy to peel, with some
easier than others. Frozen tissues were stored at -80C
until further processing. Fenton (Close lab) purified RNA
by the phenol method described in J. Japanese Soc. Hort.
Sci. 1996. 64 (4) : 809-814, purified poly(A) mRNA using a
polyA-trick mRNA isolation System IV (Promega), produced a
primary cDNA library using a Lambda ZAP XR cDNA Synthesis
Kit (Stratagene), then mass-excised one million pfu from
the primary library to produce a phagemid population.
Phagemids were plated, plasmid DNA purified, cDNA clones
archived, and DNA sequences determined bi-directionally
using an ABI3730 at the Arizona Genomics Institute,
University of Arizona (Kim, Kudrna, Wing, Yu).
Chromatogram files were downloaded by FTP to UC Riverside
(bv Close), then processed at UC Riverside (bv Manamaker,
Close lab) using the HarvEST pipeline
(http://harvest.ucr.edu) to remove vector and cloning
oligo sequences and various contaminants, and to trim to a
high quality region. Sequences that retained a paired 17
region of at least 100 bases were deposited to GenBank."

```

```

RESULT 15
CF828592/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

```

```

1..657
/organism="Citrus reticulata"
/mol_type="mRNA"
/cultivar="Clementina Fina Sodea"
/db_xref="taxon:85571"
/clone="CR_CEA01N03"
/tissue_type="Albedo"
/dev_stage="12 year old trees"
/lab_host="E. coli TUC121"

```







Oy	61	CTTTGGCCCTGGTAGTTTGGGTGGGGGAAAGCGCGCTTCGTCCGCCAGATCGGTGGCGCGGG	120
Db	61	CTTTGGCCCTGGTAGTTTGGGTGGGGGAAAGCGCGCTTCGTCCGCCAGATCGGTGGCGCGGG	120
Oy	121	AGGGCGGGATCTCGCGGCTGGCGGTCTCCGGGGGTAGTCGGCCCGGATCTTCGCGGGGA	180
Db	121	AGGGCGGGATCTCGCGGCTGGCGGTCTCCGGGGGTAGTCGGCCCGGATCTTCGCGGGGA	180
Oy	181	ATGGGGCTCTCGGATGTAGATCTGATCCGCGGTGTGTTGGGGGAGATGATGGGGCGTTTAA	240
Db	181	ATGGGGCTCTCGGATGTAGATCTGATCCGCGGTGTGTTGGGGGAGATGATGGGGCGTTTAA	240
Oy	241	AATTTCCGCATCTAAACAAGATCAGAGAGGGGGGAAAAGGACATATGGTTATATTTT	300
Db	241	AATTTCCGCATCTAAACAAGATCAGAGAGGGGGGAAAAGGACATATGGTTATATTTT	300
Oy	301	TATATATTTCTGCTGCTCGTCAAGGCTTAGATGTGCTAGATCTTTCCTTCTCTTTT	360
Db	301	TATATATTTCTGCTGCTCGTCAAGGCTTAGATGTGCTAGATCTTTCCTTCTCTTTT	360
Oy	361	GTGGGTAGATTTTGAATTCCTCAGCAATGTTCATCGGTAGTTTTCCTTTCATGATTTGT	420
Db	361	GTGGGTAGATTTTGAATTCCTCAGCAATGTTCATCGGTAGTTTTCCTTTCATGATTTGT	420
Oy	421	GACCAATGCAAGCTGTGGGGAGCTTTTGTGAG	454
Db	421	GACCAATGCAAGCTGTGGGGAGCTTTTGTGAG	454

RESULT 2  
US-09-037-531-3  
; Sequence 3, Application US/09037531

```

?
?
? GENERAL INFORMATION:
? APPLICANT: Derose, Richard
? APPLICANT: Freysinet, Georges
? TITLE OF INVENTION: Maize H3C4 Promoter Combined With The
? TITLE OF INVENTION: First Intron Of Rice Actin, Chimeric Gene Comprising It
? TITLE OF INVENTION: And Transformed Plant
? NUMBER OF SEQUENCES: 5
? CORRESPONDENCE ADDRESS:
?
```

ADDRESSEE: Connolly, Bove, Lodge, & Hutz  
STREET: 1220 Market Street  
CITY: Wilmington  
STATE: DE  
COUNTRY: USA

```

?      COMPUTER READABLE FORM.
?
?      MEDIUM TYPE:  Floppy disk
?
?      COMPUTER:      IBM PC compatible
?
?      OPERATING SYSTEM:  PC-DOS/MS-DOS
?
?      SOFTWARE:  Patent'n Release #1.0, Version #1.25
?

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/037,531
; FILING DATE: 10-MAR-1998
;

```

CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: McMorrow Jr Robert C

REGISTRATION NUMBER: 30962  
REFERENCE/DOCKET NUMBER: 5500\*24

TELECOMMUNICATION INFORMATION  
TELEPHONE: (302) 658-9141  
INFORMATION FOR SEQ ID NO: 3:

```

SEQUENCE CHARACTERISTICS:
LENGTH: 1565 base pairs

```

```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;

```

MOLECULE TYPE: DNA (genomic)  
US-09-037-531-3

Query Match	100.0%;	Score 454;	DB 4;	Length 1565;
Best Local Similarity	100.0%;	Pred. No. 4.3e-211;		

[illegible]

RESULT 3  
US-09-078-862-5  
; Sequence 5, Application US/09078862  
Reference No. 0001003

1 PATENT NO.: 8091003  
2  
3 GENERAL INFORMATION:  
4 APPLICANT: Nan, Guo-Ling  
5 APPLICANT: Nagai, Chitumi  
6 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENETIC  
7 TITLE OF INVENTION: TRANSFORMATION OF PINEAPPLE  
8 NUMBER OF SEQUENCES: 6  
9  
10 CORRESPONDENCE ADDRESS: 11

;;  
;; ADDRESS: Medien & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
;;

```

; STATE: California
; COUNTRY: United States of America
; ZIP: 94104

```

```

; ZIF: 31104
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
;

```

```

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/078,862

;; FILING DATE: 14-MAY-1998  
;; CLASSIFICATION: 800  
;; ATTORNEY/AGENT INFORMATION:

NAME: Carroll, Peter G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: IH-03321

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 5  
SEQUENCE CHARACTERISTICS:

LENGTH: 623 base pairs  
TYPE: nucleic acid

```

/          0.25 base pair
;          TYPE: nucleic acid
;          STRANDEDNESS: double
;

```

```

;          TOPOLOGY: circular
;          MOLECULE TYPE: other nucleic acid
;          DESCRIPTION: /desc = "DNA"
US-09-078-862-5

```

Query Match	64.1%	Score 291;	DB 3;	Length 623;
Best Local Similarity	100.0%	Pred. NC.	8.8e-1324	
Matches 291;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	164	CCGATCCTCGCGGGAAATGGGGCTCTGGATGTGATCTCATCGCGCTGTGTGGGGA	223
Db	278	CCGATCCTCGCGGGAAATGGGGCTCTGGATGTGATCTCATCGCGCTGTGTGGGGA	337
QY	224	GATGATGGGGCGTTAAAAATTTCCGCAATGCTPAAACAGATCAGGAAGGGGAAAAGGCG	283
Db	338	GATATGGGGCGTTAAAAATTTCCGCAATGCTPAAACAGATCAGGAAGGGGAAAAGGCG	397
QY	284	ACTATGGTTATATTTTATATATTTCTGCTGCTGCTGTCAGGCTTAGATGTGTAGAT	343
Db	398	ACTATGGTTATATTTTATATATTTCTGCTGCTGCTGTCAGGCTTAGATGTGTAGAT	457
QY	344	CTTTCCTTCTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCATTTTCATCGTAGTTT	403
Db	458	CTTTCCTTCTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCATTTTCATCGTAGTTT	517
QY	404	TTCTTTTCATGATTTTGACAAATGCAACCTCTGTGGGAGCTTTTGTAG	454
Db	518	TTCTTTTCATGATTTTGACAAATGCAACCTCTGTGGGAGCTTTTGTAG	568

```

RESULT 4
US-08-144-602B-6
/ Sequence 6, Application US/08144602B
/ Patent No. 5641876
/ GENERAL INFORMATION:
/ APPLICANT: MCELROY, David
/ APPLICANT: Wu, Ray
/ TITLE OF INVENTION: RICE ACTIN GENE AND PROMOTER
/ NUMBER OF SEQUENCES: 27
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
/ STREET: CLINTON SQUARE, P.O. BOX 1051
/ CITY: ROCHESTER
/ STATE: NEW YORK
/ COUNTRY: USA
/ ZIP: 14603
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/144,602B
/ FILING DATE: 27-OCT-1993
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: TIMIAN, SUSAN J.
/ REGISTRATION NUMBER: 34,103
/ REFERENCE/DOCKET NUMBER: 19603/10140
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 716-263-1636
/ TELEFAX: 716-263-1600
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1392 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: CDNA
/
/ US-08-144-602B-6
Query Match 64.1%; Score 291; DB 1; Length 1392;
Best Local Similarity 100.0%; Freq. No. 8; 8e-132;

```

	Matches	291;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
OY	164	CCGGATCTTCGCGGGGAATTGGGCTCTCAGATGTAGAATCTGCATCCGCCGTTTGTGGGGGA	223							
Dδ	1076	CCGGATCTTCGCGGGGAATGGGCTCTCAGATGTAGAATCTGCATCCGCCGTTTGTGGGGGA	1135							
OY	224	GATGATGGGGCGTTTTAAATTTTGCCCATGCTAACAAGATCAGAMAGGGGAAAAGGC	283							
Dδ	1136	GATGATGGGGCGTTTTAAATTTTGCCCATGCTAACAAGATCAGAMAGGGGAAAAGGC	1195							
OY	284	ACATAGTTTAATTTTTTAATAATTTGCTGCTGCTGCATGCAAGCTTAGATAGTACTGAT	343							
Dδ	1196	ACATAGTTTAATTTTTTAATAATTTGCTGCTGCTGCATGCAAGCTTAGATAGTACTGAT	1255							
OY	344	CYTTCCTTCTCTTTTGTGGGAGAAATTGAATCCTCAGACATGTTCATCGGTAGTTT	403							
Dδ	1256	CYTTCCTTCTCTTTTGTGGGAGAAATTGAATCCTCAGACATGTTCATCGGTAGTTT	1315							
OY	404	TTCCTTTCAGATTTTGACAAATGCAAGCCTCGGCGGAGACTTTTGTGAG	454							
Dδ	1316	TTCCTTTCAGATTTTGACAAATGCAAGCCTCGGCGGAGACTTTTGTGAG	1366							

```

RESULT 5
US-08-144-602B-7
/ Sequence 7, Application US/08144602B
/ Patent No. 5641876
/ GENERAL INFORMATION:
/ APPLICANT: McElroy, David
/ APPLICANT: Wu, Ray
/ TITLE OF INVENTION: RICE ACTIN GENE AND PROMOTER
/ NUMBER OF SEQUENCES: 27
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
/ STREET: CLINTON SQUARE, P.O. BOX 1051
/ CITY: ROCHESTER
/ STATE: NEW YORK
/ COUNTRY: USA
/ ZIP: 14603
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/144,602B
/ FILING DATE: 27-OCT-1993
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: TIMIAN, SUSAN J.
/ REGISTRATION NUMBER: 34,103
/ REFERENCE/DOCKET NUMBER: 19603/10140
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 716-263-1636
/ TELEFAX: 716-263-1600
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1404 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-08-144-602B-7

Query Match          64.1%; Score 291; DB 1; Length 1404;
Best Local Similarity 100.0%; Pred.No.8.8e-132;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      164      CCGGATCTCGCGGGGATGGGCTCTCGGATGTAGATCGGCGCTGTTGGGGGA 223
          |||||
Db      1086      CCGGATCTCGCGGGGATGGGCTCTCGGATGTAGATCGGCGCTGTTGGGGGA 1145
Oy      224      GATGATGGGCGTTTAAATTTGCCATGCTAAACAAGATCAGAGAGGGGAAAAGGC 283

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Db	1146	GATGATGGGGCTTTAAATTTCCGCACTCTAAACAATATGAGAAAGGGGAAAAGGC	1205
Qy	284	ACTATGGTTTATATTTATATATTTCTGCTCTGCTGCTCAGGCTTATGATGTCTATAT	343
Db	1206	ACTATGGTTTATATTTATATATTTCTGCTCTGCTGCTCAGGCTTATGATGTCTATAT	1255
Qy	344	CTTCTTTCTTCTTTTGTGGTAGAATTTGAATCCCTCAGCATTTGTCATCGTAGTTT	403
Db	1266	CTTCTTTCTTCTTTTGTGGTAGAATTTGAATCCCTCAGCATTTGTCATCGTAGTTT	1325
Qy	404	TTCTTTTCATGATTTGTGACAAATGCAGCTCTGTGCGGAGCTTTTGTAG	454
Db	1326	TTCTTTTCATGATTTGTGACAAATGCAGCTCTGTGCGGAGCTTTTGTAG	1376

```

1      RESULT 6
2      US-08-144-602B-5
3      : Sequence 5, Application US/08144602B
4      : Patent No. 5641876
5      : GENERAL INFORMATION:
6      : APPLICANT: McELROY, David
7      : APPLICANT: Wu, Ray
8      : TITLE OF INVENTION: RICE ACTIN GENE AND PROMOTER
9      : NUMBER OF SEQUENCES: 27
10     : CORRESPONDENCE ADDRESS:
11     : ADDRESSEE: NIKON, HARGRAVE, DEVANS & DOYLE LLP
12     : STREET: CLINTON SQUARE, P.O. BOX 1051
13     : CITY: ROCHESTER
14     : STATE: NEW YORK
15     : COUNTRY: USA
16     : ZIP: 14603
17     : COMPUTER READABLE FORM:
18     : MEDIUM TYPE: Floppy disk
19     : COMPUTER: IBM PC compatible
20     : OPERATING SYSTEM: PC-DOS/MS-DOS
21     : SOFTWARE: PatentIn Release #1.0, Version #1.30
22     : CURRENT APPLICATION DATA:
23     : APPLICATION NUMBER: US/08/144,602B
24     : FILING DATE: 27-OCT-1993
25     : CLASSIFICATION: 536
26     : ATTORNEY/AGENT INFORMATION:
27     : NAME: TIMIAN, SUSAN J.
28     : REGISTRATION NUMBER: 34,103
29     : REFERENCE/DOCKET NUMBER: 19603/10140
30     : TELECOMMUNICATION INFORMATION:
31     : TELEPHONE: 716-263-1636
32     : TELEFAX: 716-263-1600
33     : INFORMATION FOR SEQ ID NO: 5:
34     : SEQUENCE CHARACTERISTICS:
35     : LENGTH: 2199 base pairs
36     : TYPE: nucleic acid
37     : STRANDEDNESS: single
38     : TOPOLOGY: linear
39     : MOLECULE TYPE: CDNA
40     :
41     : US-08-144-602B-5

```

Query Match	64.1%	Score 291	DB 1	Length 2199
Best Local Similarity	100.0%	Pred. No. 8.9e+132		
Matches 291	Conservative 0	Mismatches 0	Gaps 0	

QY	164	CGAGTCCGCGGGGAAATGGGGCTCTGGAGATGTAGATCGCCGTTTGGGGGGA	223
Db	1883	CCGAGTCCGCGGGGAAATGGGGCTCTGGAGATGTAGATCGCCGTTTGGGGGGA	1947
QY	224	GATGATGGGGCGTTTAAATTTCCGCATGCTTAAACAGATCAGAGAGGGGAAAAAGGC	283
Db	1943	GATGATGGGGCGTTTAAATTTCCGCATGCTTAAACAGATCAGAGAGGGGAAAAAGGC	2007
QY	284	ACTATGTTTAAATTTTAAATATATTTTCGCTGCTCGTCAGGCTTATGATGTGCTAGAT	343
Db	2003	ACTATGTTTAAATTTTAAATATATTTTCGCTGCTCGTCAGGCTTATGATGTGCTAGAT	2066

OY	344	CTTCTTTCCTCTTTTGTGGGTGAAATTGAATCCCTCAGCATGTTCATCGGTAGTTT	403
Db	2063	CTTCTTTCCTCTTTTGTGGGTGAAATTGAATCCCTCAGCATGTTCATCGGTAGTTT	2122
OY	404	TTCTTTTCAGATTGTGACAAATGACGACCTCGTGCAGGATCTTTTGTAG	454
Db	2123	TTCTTTTCAGATTGTGACAAATGACGACCTCGTGCAGGATCTTTTGTAG	2173

```

1      RESULT 7
2      US-08-144-602B-4
3      ; Sequence 4, Application US/080144602B
4      ; Patent No. 5641876
5      ; GENERAL INFORMATION:
6      ; APPLICANT: MCELROY, David
7      ; APPLICANT: Wu, Ray
8      ; TITLE OF INVENTION: RICE ACTIN GENE AND PROMOTER
9      ; NUMBER OF SEQUENCES: 27
10     ; CORRESPONDENCE ADDRESS:
11     ; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
12     ; STREET: CLINTON SQUARE, P.O. BOX 1051
13     ; CITY: ROCHESTER
14     ; STATE: NEW YORK
15     ; COUNTRY: USA
16     ; ZIP: 14603
17     ; COMPUTER READABLE FORM:
18     ; MEDIUM TYPE: Floppy disk
19     ; COMPUTER: IBM PC compatible
20     ; OPERATING SYSTEM: PC-DOS/MS-DOS
21     ; SOFTWARE: PatentIn Release #1.0, Version #1.30
22     ; CURRENT APPLICATION DATA:
23     ; APPLICATION NUMBER: US/08/144,602B
24     ; FILING DATE: 27-OCT-1993
25     ; CLASSIFICATION: 536
26     ; ATTORNEY/AGENT INFORMATION:
27     ; NAME: TIMJIAN, SUSAN J.
28     ; REGISTRATION NUMBER: 34,103
29     ; REFERENCE/DOCKET NUMBER: 19603/10140
30     ; TELECOMMUNICATION INFORMATION:
31     ; TELEPHONE: 716-263-1606
32     ; TELEFAX: 716-263-1600
33     ; INFORMATION FOR SEQ ID NO: 4:
34     ; SEQUENCE CHARACTERISTICS:
35     ; LENGTH: 5643 base pairs
36     ; TYPE: nucleic acid
37     ; STRANDEDNESS: single
38     ; TOPOLOGY: linear
39     ; MOLECULE TYPE: cDNA
40     ;
41     ; US-08-144-602B-4

```

Query Match 291; Score 291; DB 1; Length 5643; 64.1%;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-133;  
 Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY	164	CCGATCCTCCGCGGGGATGGGGCTTCGATGTAGATCTATCCGCGTGTGTGGGGGA	223
Db	1886	CCGATCCTCCGCGGGGATGGGGCTTCGATGTAGATCTATCCGCGTGTGTGGGGGA	1945
QY	224	GATGATGGGGCGTTAAATTTCCGCATCTAAACAGATCAGGAAGGGGAAAAAGGC	283
Db	1946	GATGATGGGGCGTTAAATTTCCGCAGCTAAACAGATCAGGAAGGGGAAAAAGGC	2003
QY	284	ACTATGGTTATATTTATATATTTCTGCTGCTGCTGTCAGCGTTATGATGTCTAGAT	343
Db	2006	ACTATGGTTATATTTATATATTTCTGCTGCTGCTGTCAGCGTTATGATGTCTAGAT	2065
QY	344	CTTTCCTTCTCTTTTGTGGGTAGAAATTGAATCCCTCAGCATTTGTCATCGTAGATT	403
Db	2066	CTTTCCTTCTCTTTTGTGGGTAGAAATTGAATCCCTCAGCATTTGTCATCGTAGATT	2125
QY	404	TTCTTTTATGATTTGTGACAAATGCGAGCCTCGTGGGAGGTTTTTSTAG	454
Db	2126	TTCTTTTATGATTTGTGACAAATGCGAGCCTCGTGGGAGGTTTTTSTAG	2176

```

RESULT 8
US-09-377-466B-19
: Sequence 19, Application US/09377466B
: Patent No. 6501009
: GENERAL INFORMATION:
: APPLICANT: Romano, Charles P.
: TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
: FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
: CURRENT APPLICATION NUMBER: US/09/377,466B
: CURRENT FILING DATE: 1999-08-19
: NUMBER OF SEQ ID NOS: 43
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 19
: LENGTH: 3039
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURES:
: OTHER INFORMATION: Description of Artificial Sequence: expression
: NAME/KEY: Promoter
: LOCATION: (14)..(235)
: OTHER INFORMATION: P-CaMV.AS4
: NAME/KEY: 5'UTR
: LOCATION: (240)..(304)
: OTHER INFORMATION: L-Ta.hcb1
: NAME/KEY: Intron
: LOCATION: (318)..(805)
: OTHER INFORMATION: I-Os.Act1
: NAME/KEY: CDS
: LOCATION: (811)..(2769)
: OTHER INFORMATION: Cry3Bb1 variant 11231mv1
: NAME/KEY: terminator
: LOCATION: (2787)..(3020)
: OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-19

Query Match 29.7%; Score 135; DB 4; Length 3039;
Best Local Similarity 100.0%; Pred. No. 7,2e-56;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 TCGTCAGGCGTTAGATGCTAGATCTTCTCTCTTTGGGTAGAAATTGAATCC 379
Db 660 TCGTCAGGCGTTAGATGCTAGATCTTCTCTCTTTGGGTAGAAATTGAATCC 719

QY 380 CTCAGCATTCGTATCGGTAGTTTCTTTCATGATTTGTGCAAAATGACAGCTCGTGC 439
Db 720 CTCAGCATTCGTATCGGTAGTTTCTTTCATGATTTGTGCAAAATGACAGCTCGTGC 779

QY 440 GGAGCTTTTGTGAG 454
Db 780 GGAGCTTTTGTGAG 794

RESULT 9
US-09-377-466B-21
: Sequence 21, Application US/09377466B
: Patent No. 6501009
: GENERAL INFORMATION:
: APPLICANT: Romano, Charles P.
: TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
: FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
: CURRENT APPLICATION NUMBER: US/09/377,466B
: CURRENT FILING DATE: 1999-08-19
: NUMBER OF SEQ ID NOS: 43
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 21
: LENGTH: 3039
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURES:
: OTHER INFORMATION: Description of Artificial Sequence: expression

```

```

OTHER INFORMATION: cassette
NAME/KEY: promoter
LOCATION: (14)..(235)
OTHER INFORMATION: P-CamV.AS4
NAME/KEY: 5' UTR
LOCATION: (240)..(304)
OTHER INFORMATION: L-Ta.hcb1
NAME/KEY: intron
LOCATION: (318)..(805)
OTHER INFORMATION: I-Or.Act1
NAME/KEY: CDS
LOCATION: (811)..(2769)
OTHER INFORMATION: Cry3Bb1 variant 11231mw2
NAME/KEY: terminator
LOCATION: (2787)..(3020)
OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-21

Query Match          29.7%! Score 135; DB 4; Length 3039;
Best Local Similarity 100.0%! Pred. No. 7.2e-56;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      320 TCCTCAGGCTTAGATGTCAGATCTTTCTTCTTTTGTGGTAGAAATTGAATCC 379
Db       660 TCCTCAGGCTTAGATGTCAGATCTTTCTTCTTTTGTGGTAGAAATTGAATCC 719
          |||
QY      380 CTCAGATTGTCATCGTAGTCTTTCTTTTCATGATTTTGACAATGACGCTCGTCC 439
Db       720 CTCAGATTGTCATCGTAGTCTTTCTTTTCATGATTTTGACAATGACGCTCGTCC 779
          |||
QY      440 GGAGCTTTTGTGAG 454
Db       780 GGAGCTTTTGTGAG 794
          |||

RESULT 10
US-09-377-466B-38
; Sequence 38, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OR INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 3044
; TYPE: DNA
; ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: expression
OTHER INFORMATION: cassette
NAME/KEY: promoter
LOCATION: (14)..(235)
OTHER INFORMATION: P-CamV.AS4
NAME/KEY: 5' UTR
LOCATION: (240)..(304)
OTHER INFORMATION: L-Ta.hcb1
NAME/KEY: intron
LOCATION: (318)..(805)
OTHER INFORMATION: I-Or.Act1
NAME/KEY: CDS
LOCATION: (811)..(2769)
OTHER INFORMATION: variant Cry3Bb1 coding sequence encoding v11231
NAME/KEY: terminator
LOCATION: (2792)..(3025)
OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-38

Query Match          29.7%! Score 135; DB 4; Length 3044;
Best Local Similarity 100.0%! Pred. No. 7.2e-56;

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Matches	135; Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	320	TCGTCAGGCTTAGAGTGTCTAGATCTTTCTTTCTTTTGTGGGTAGATTTGAATCC	379					
Db	660	TCGTCAGGCTTAGAGTGTCTAGATCTTTCTTTCTTTTGTGGGTAGATTTGAATCC	719					
QY	380	CTCAGCATTTCTCATCGGTATGTTTTCTTTTCATGATTTGTACAAATGCACCTCGTGC	439					
Db	720	CTCAGCATTTCTCATCGGTATGTTTTCTTTTCATGATTTGTACAAATGCACCTCGTGC	779					
QY	440	GGAGCTTTTTTTGTAG	454					
Db	780	GGAGCTTTTTTTGTAG	794					
<p>RESULT 11</p> <p>US-09-377-466B-17</p> <p>Sequence 17, Application US/09377466B</p> <p>Patent No. 6501009</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Romano, Charles P.</p> <p>TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants</p> <p>FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn</p> <p>CURRENT FILING DATE: 1999-08-19</p> <p>NUMBER OF SEQ ID NOS: 43</p> <p>SOFTWARE: PatentIn Ver. 2.0</p> <p>SEQ ID NO 17</p> <p>LENGTH: 3450</p> <p>TYPE: DNA</p> <p>ORGANISM: Artificial Sequence</p> <p>FEATURE:</p> <p>OTHER INFORMATION: Description of Artificial Sequence: expression</p> <p>NAME/KEY: promoter</p> <p>LOCATION: (14)..(235)</p> <p>OTHER INFORMATION: P-CamV.AS4</p> <p>NAME/KEY: 5' UTR</p> <p>LOCATION: (240)..(304)</p> <p>OTHER INFORMATION: L-Ta.hcb1</p> <p>NAME/KEY: intron</p> <p>LOCATION: (318)..(805)</p> <p>OTHER INFORMATION: I-Os.Act1</p> <p>NAME/KEY: transit peptide</p> <p>LOCATION: (825)..(971)</p> <p>OTHER INFORMATION: amino terminal TS-Zm.rbcS</p> <p>NAME/KEY: intron</p> <p>LOCATION: (972)..(1134)</p> <p>OTHER INFORMATION: I-Zm.rbcS</p> <p>NAME/KEY: transit peptide</p> <p>LOCATION: (1135)..(1221)</p> <p>OTHER INFORMATION: carboxy terminus TS-Zm.rbcS</p> <p>NAME/KEY: CDS</p> <p>LOCATION: (1222)..(3180)</p> <p>OTHER INFORMATION: Cry3Bb1 variant 1123imv1</p> <p>NAME/KEY: terminator</p> <p>LOCATION: (3198)..(3431)</p> <p>OTHER INFORMATION: T-Ta.hsp17</p> <p>US-09-377-466B-17</p>								
QY	320	TCGTCAGGCTTAGAGTGTCTAGATCTTTCTTTCTTTTGTGGGTAGATTTGAATCC	379					
Db	660	TCGTCAGGCTTAGAGTGTCTAGATCTTTCTTTCTTTTGTGGGTAGATTTGAATCC	719					
QY	380	CTCAGCATTTCTCATCGGTATGTTTTCTTTTCATGATTTGTACAAATGCACCTCGTGC	439					
Db	720	CTCAGCATTTCTCATCGGTATGTTTTCTTTTCATGATTTGTACAAATGCACCTCGTGC	779					
QY	440	GGAGCTTTTTTTGTAG	454					
Db	780	GGAGCTTTTTTTGTAG	794					
<p>Query Match 29.7%; Score 135; DB 4; Length 3450;</p> <p>Best Local Similarity 100.0%; Pred. No. 7.2e-56;</p> <p>Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>								

```

Db          780 GGAGCTTTTGTG 794
|||||
RESULT 12
US-09-377-466B-36
; Sequence 36, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 3455
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; OTHER INFORMATION: cassette
; NAME/KEY: Promoter
; LOCATION: (14)..(235)
; OTHER INFORMATION: P.CamV.AS4
; NAME/KEY: 5'UTR
; LOCATION: (240)..(304)
; OTHER INFORMATION: L-Ta.hcb1
; NAME/KEY: intron
; LOCATION: (318)..(805)
; OTHER INFORMATION: I-Os.Act1
; NAME/KEY: transit peptide
; LOCATION: (825)..(971)
; OTHER INFORMATION: TS-Zm.rbcs amino terminal coding sequence upstream
; OTHER INFORMATION: of Zea mays rbcs intron
; NAME/KEY: intron
; LOCATION: (972)..(1134)
; OTHER INFORMATION: I-Zm.rbcs
; NAME/KEY: transit peptide
; LOCATION: (1135)..(1221)
; OTHER INFORMATION: TS-Zm.rbcs carboxy terminus coding sequence
; OTHER INFORMATION: downstream of Zea mays rbcs intron
; NAME/KEY: CDS
; LOCATION: (1222)..(3180)
; OTHER INFORMATION: Variant Cry3Bb1 coding sequence encoding v11231
; NAME/KEY: terminator
; LOCATION: (3198)..(3431)
; OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-36

Query Match      29.7%; Score 135; DB 4; Length 3455;
Best Local Similarity 100.0%; Pred. No. 7,2e-56;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY    320 TCCTCAGCGCTTAAGATGCTAGAATCTTTCTTTCTTTTGGGTAGAAATTGAATCC 379
DB    660 TCGTCAGAGCTTAGATGCTAGATCTTCTTTCTTTTGCGGTAGAAATTGAATCC 719
QY    380 CTCAGCAATGTCATCGGTATTTCTTTCTTTCAATTTGTGACAAAGCAGCTCGTGC 439
DB    720 CTCAGCAATGTCATCGGATTTTTCTTTCTTTCAATGATGTGACAAATCAGCTCGTGC 779
QY    440 GGAGCTTTTGTGAG 454
DB    780 GGAGCTTTTGTGAG 794

RESULT 13
US-09-377-466B-23
; Sequence 23, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
```

```

; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 3469
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; NAME/KEY: cassette
; LOCATION: (25)..(640)
; OTHER INFORMATION: P-CamV.35S
; NAME/KEY: 5'UTR
; LOCATION: (664)..(734)
; OTHER INFORMATION: L-Ta.hcb1
; NAME/KEY: Intron
; LOCATION: (748)..(1238)
; OTHER INFORMATION: I-0s.Accl1
; NAME/KEY: CDS
; LOCATION: (1241)..(3199)
; OTHER INFORMATION: Cry3Bb1 variant.11231mv2
; NAME/KEY: terminator
; LOCATION: (3217)..(3450)
; OTHER INFORMATION: T-Ta.hsp17
; US-09-377-466B-23

```

```

Query Match          29.7%; Score 135; DB 4; Length 3469;
Best Local Similarity 100.0%; Pred. No. 7.2e-56;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      320  TCGTCAGGCTTAAGTGTCTAGATCTTCTCTCTTTTGTGGGTAGATTGAAATCC 379
          |||
DB      1090  TCGTCAGGCTTAAGTGTCTAGATCTTCTCTCTTTTGTGGGTAGATTGAAATCC 1149
          |||
QY      380  CTCAGATTGTTGATGCGTAGTCTTCTTTTCATGATTGTGACAAATGACGCTGTGC 439
          |||
DB      1150  CTCAGATTGTTGATGCGTAGTCTTCTTTTCATGATTGTGACAAATGACGCTGTGC 1209
          |||
QY      440  GGAGCTTTTGTAG 454
          |||
DB      1210  GGAGCTTTTGTAG 1224
          |||

```

```

RESULT 14
US-09-068-101-5
; Sequence 5, Application US/09068101
; Patent No. 6372960
; GENERAL INFORMATION:
; APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Improved Barstar Gene
; FILE REFERENCE: 2121-139P
; CURRENT APPLICATION NUMBER: US/09/068, 101
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: EP 96202446.9
; EARLIER FILING DATE: 1996-09-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4032
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: other nucleic
; OTHER INFORMATION: acid, "plasmid pmv71"
; NAME/KEY: misc feature
; LOCATION: (1995)..(3400)
; OTHER INFORMATION: label = PRACT, "promoter region of rice actin gene"

```

```

; OTHER INFORMATION: - contains an intron in the leader"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3401)..(3676)
; OTHER INFORMATION: label = barstar, "barstar DNA"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3677)..(4003)
; OTHER INFORMATION: label = 3'nos, "region containing 3' untranslated
; OTHER INFORMATION: end of nopaline synthase gene of Agrobacterium
; OTHER INFORMATION: T-DNA"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3399)..(3404)
; OTHER INFORMATION: label = NcoI, "NcoI recognition site"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4015)..(4021)
; OTHER INFORMATION: label = KpnI, "KpnI recognition site"
; US-09-068-101-5

```

```

Query Match          29.7%; Score 135; DB 3; Length 4032;
Best Local Similarity 100.0%; Pred. No. 7.2e-56;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      320  TCGTCAGGCTTAAGTGTCTAGATCTTCTCTCTTTTGTGGGTAGATTGAAATCC 379
          |||
DB      3259  TCGTCAGGCTTAAGTGTCTAGATCTTCTCTCTTTTGTGGGTAGATTGAAATCC 3318
          |||
QY      380  CTCAGATTGTTGATGCGTAGTCTTCTTTTCATGATTGTGACAAATGACGCTGTGC 439
          |||
DB      3319  CTCAGATTGTTGATGCGTAGTCTTCTTTTCATGATTGTGACAAATGACGCTGTGC 3378
          |||
QY      440  GGAGCTTTTGTAG 454
          |||
DB      3379  GGAGCTTTTGTAG 3393
          |||

```

```

RESULT 15
US-09-970-921-5
; Sequence 5, Application US/09970921
; Patent No. 6758575
; GENERAL INFORMATION:
; APPLICANT: Frank Michiels et al.
; TITLE OF INVENTION: Improved Barstar Gene
; FILE REFERENCE: 2428-0108P
; CURRENT APPLICATION NUMBER: US/09/970,921
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4032
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: other nucleic
; OTHER INFORMATION: acid, "plasmid pmv71"
; NAME/KEY: misc feature
; LOCATION: (1995)..(3400)
; OTHER INFORMATION: label = PRACT, "promoter region of rice actin gene
; OTHER INFORMATION: - contains an intron in the leader"
; NAME/KEY: misc feature
; LOCATION: (3401)..(3676)
; OTHER INFORMATION: label = barstar, "barstar DNA"
; NAME/KEY: misc feature
; LOCATION: (3677)..(4003)
; OTHER INFORMATION: label = 3'nos, "region containing 3' untranslated
; OTHER INFORMATION: end of nopaline synthase gene of Agrobacterium
; OTHER INFORMATION: T-DNA"
; NAME/KEY: misc feature
; LOCATION: (3395)..(3404)
; OTHER INFORMATION: label = NcoI, "NcoI recognition site"
; NAME/KEY: misc feature

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 11:40:58 ; Search time 240.829 Seconds  
(without alignments)  
12380.260 Million cell updates/sec

Title: US-10-758-799-2

Perfect score: 454  
Sequence: 1 GTTACACACCCGCCCTCTC.....CGTGGAGCTTTTGTAG 454

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 7351250 seqs, 3283620254 residues

Word size : 0

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications NA:\*

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19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq:\*

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21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:\*

22: /cgn2\_6/ptodata/1/pubpna/US10I\_NEW\_PUB.seq:\*

23: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

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26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	454	100.0	454	9	US-09-037-531-2
2	454	100.0	454	19	US-10-758-799-2
3	454	100.0	1565	9	US-09-037-531-3
4	454	100.0	1565	19	US-10-758-799-3
5	291	64.1	623	9	US-09-981-9008-19
6	289	63.7	470	16	US-10-087-167-109
7	203	44.7	1259	10	US-09-991-209-43

8	203	44.7	4773	10	US-09-991-209-32	Sequence 32, Appl
9	203	44.7	4950	10	US-09-991-209-34	Sequence 34, Appl
10	203	44.7	4965	10	US-09-991-209-37	Sequence 37, Appl
11	203	44.7	4974	10	US-09-991-209-35	Sequence 35, Appl
12	203	44.7	5164	10	US-09-991-209-36	Sequence 36, Appl
13	203	44.7	5277	10	US-09-991-209-25	Sequence 25, Appl
14	203	44.7	5295	10	US-09-991-209-38	Sequence 38, Appl
15	203	44.7	5327	10	US-09-991-209-27	Sequence 27, Appl
16	203	44.7	5337	10	US-09-991-209-19	Sequence 19, Appl
17	203	44.7	5337	10	US-09-991-209-23	Sequence 23, Appl
18	203	44.7	5337	10	US-09-991-209-31	Sequence 31, Appl
19	203	44.7	5338	10	US-09-991-209-15	Sequence 15, Appl
20	203	44.7	5338	10	US-09-991-209-29	Sequence 29, Appl
21	203	44.7	5345	10	US-09-991-209-17	Sequence 17, Appl
22	203	44.7	5387	10	US-09-991-209-41	Sequence 41, Appl
23	203	44.7	5395	10	US-09-991-209-21	Sequence 21, Appl
24	203	29.7	491	9	US-09-376-940-50	Sequence 50, Appl
25	135	29.7	1384	22	US-10-839-092-35	Sequence 35, Appl
26	135	29.7	1597	22	US-10-839-092-50	Sequence 50, Appl
27	135	29.7	2460	21	US-10-678-588A-1	Sequence 1, Appl
28	135	29.7	3034	20	US-10-841-796-34	Sequence 34, Appl
29	135	29.7	3039	15	US-10-232-665-19	Sequence 19, Appl
30	135	29.7	3039	15	US-10-232-665-21	Sequence 21, Appl
31	135	29.7	3044	15	US-10-232-665-38	Sequence 38, Appl
32	135	29.7	3450	15	US-10-232-665-17	Sequence 17, Appl
33	135	29.7	3455	15	US-10-232-665-36	Sequence 36, Appl
34	135	29.7	3469	15	US-10-232-665-23	Sequence 23, Appl
35	135	29.7	4032	9	US-09-970-921-5	Sequence 5, Appl
36	135	29.7	5365	22	US-10-839-092-57	Sequence 57, Appl
37	135	29.7	6865	10	US-09-845-064-13	Sequence 13, Appl
38	135	29.7	7794	24	US-11-057-062-2	Sequence 2, Appl
39	135	29.7	7943	10	US-09-845-064-15	Sequence 15, Appl
40	135	29.7	8590	24	US-11-057-062-1	Sequence 1, Appl
41	135	29.7	9143	10	US-09-845-064-12	Sequence 12, Appl
42	135	29.7	9339	21	US-10-344-977A-1	Sequence 1, Appl
43	135	29.7	9359	22	US-10-344-975B-1	Sequence 1, Appl
44	135	29.7	10003	10	US-09-845-064-21	Sequence 21, Appl
45	135	29.7	10003	10	US-09-845-064-21	Sequence 21, Appl

#### ALIGNMENTS

RESULT 1  
US-09-037-531-2  
Sequence 2, Application US/09037531  
Patent No. US20020104117A1  
GENERAL INFORMATION:  
APPLICANT: Derose, Richard  
TITLE OF INVENTION: Freysinet, Georges  
TITLE OF INVENTION: Maize H3C4 Promoter Combined With The  
TITLE OF INVENTION: First Region Of Rice Actin, Chimeric Gene Comprising It  
TITLE OF INVENTION: And Transformed Plant  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Connolly, Bove, Lodge, & Hutz  
STREET: 1220 Market Street  
CITY: Wilmington  
STATE: DE  
COUNTRY: USA  
ZIP: 19899  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/037,531  
FILING DATE: 10-MAR-1998  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: McMorrow Jr., Robert G.  
REGISTRATION NUMBER: 30962





Query Match	64.1%;	Score 291;	DB 9;	Length 623;
Best Local Similarity	100.0%;	Pred. No. 2.3e-139;		
Matches 291;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

ESULT 6  
S-10-087-167-109

ORGANISM: *Oryza sp.*  
S-10-087-167-109

166 GATCCTCGCGGGAATGGGGCTCTGGAGTAGATCTGAATCCGCCGTGTTGGGGGAGA 225

RESULT 7  
S-09-991-209-43

Query Match	44.7%	Score 203;	DB 10;	length 1259;
Best Local Similarity	100.0%;	Pred. No. 5.4e-94;		
Matches 203;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

1109 ATGGGCTCTCGGATGTAGATCT 1131

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RESULT 9
US-09-991-209-34
; Sequence 34, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; FILE REFERENCE: GGC48-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 4950
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pU06.1 vector
US-09-991-209-34

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Query Match	44.7%	Score 203;	DB 10;	Length 4965;
Best local Similarity	100.0%;	Pred. No. 5, 6e-94;		
Matches 203;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GINACCACCCCGCCCTCTCTCTTTCTTCTCCGTTTTTTTTTGGTCTCGAT	60	
Db	537	GTACCAACCCCGCCCTCTCTCTTTCTTCTCCGTTTTTTTTTGGTCTCGAT	596	
QY	61	CTTTGGCCTTTGAGTTTGGGTGGGAGAGGGGCTTCGTGGCCAGATGCGTGGCGGG	120	
Db	597	CTTTGGCCTTTGAGTTTGGGTGGGAGAGGGGCTTCGTGGCCAGATGCGTGGCGGG	656	
QY	121	AGGGGCGGGAATCTCGCGGCTGAGGCTCTCGGGGCGTGAAGTGGCCCGGATCTCGCGGGA	180	
Db	657	AGGGGCGGGAATCTCGCGGCTGAGGCTCTCGGGGCGTGAAGTGGCCCGGATCTCGCGGGA	716	
QY	181	ATGGGGCTCTCGGATGTAGATCT	203	
Db	717	ATGGGGCTCTCGGATGTAGATCT	739	

RESULT 11

US-09-991-209-35

; Sequence 35, Application US/09991209

; Publication No. US20030024009A1

; GENERAL INFORMATION:

```

1  APPLICANT: Dunn-Coleman, Nigel
2  APPLICANT: Langdon, Timothy
3  APPLICANT: Morse, Philip
4  TITLE OF INVENTION: Manipulation of the Phenolic Acid
5  TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
6  TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
7  FILE REFERENCE: GCG48-2
8  CURRENT APPLICATION NUMBER: US/09/991,209
9  CURRENT FILING DATE: 2002-07-02
10 PRIOR APPLICATION NUMBER: US 60/249,608
11 PRIOR FILING DATE: 2000-11-17
12 NUMBER OF SEQ ID NOS: 97
13 SOFTWARE: FastSeq for Windows Version 4.0
14 SEQ ID NO 35
15 LENGTH: 4974
16 TYPE: DNA
17 ORGANISM: Artificial Sequence
18 FEATURE:
19 OTHER INFORMATION: pUD4 vector
20 US-09-991-209-35

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Query Match      44.7%; Score 203; DB 10; Length 4974;
Best Local Similarity 100.0%; Pred. No. 5.6e-94;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 GTAACCAACCCGCCCCCTCTCTCTCTCTCTCTCGGTTTTTTTTTTTCGTCCTCGGTCCTCGAT 60

61 CTTGGCCCTTGGTACCTTGGGTGGCGAGAGCGGCTTCGTGCGCCAGATCGGTGGCGGGG 120

121 AGGGGGGGGATCTGGCGGCTGCGCTCTCCGGGCGTAGTCCGCCCCGATCCTCGCGGGGA 180

181 ATGGGGCTCTCGGATGATCT 203

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RESULT 12
US-09-991-209-36
; Sequence 36, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Philip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: G0448-2
; CURRENT APPLICATION NUMBER: US/09/991, 209
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249, 608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 5164
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pPQ10.1 vector
US-09-991-209-36

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Query Match	44.7%	Score 203	DB 10	Length 5154
Best Local Similarity	100.0%	Pred. No. 5.6e-94		
Matches 203; Conservative	0	Mismatches	0	Indels
0	Gaps			
by	1	GTAAACACCCGCCCTCTCTCTTTCTTTTCCGTTTTTTTTTTTGGTCGCGCTCGAT	60	

Accession	Sequence	Position
Db	GTACCAACCCCGCCCTCTCTCTTCTTCTCGCTTTTTTTTCTGCTCGATCGAT	490
Qy	CTTTGACCTTGTAGTTTGGGTGGCGAAGCGCTTGTGCGCCAGATCGTGGCGGG	120
Db	CTTTGGCTTTGTAGTTTGGGTGGCGAAGCGCTTGTGCGCCAGATCGTGGCGGG	496
Qy	AGGGCGGGATCTCGCGGCTGGCGCTTCCGGCGTGAATCGGCCCGGATCTTCGCGGGGA	180
Db	AGGGCGGGATCTCGCGGCTGGCGCTTCCGGCGTGAATCGGCCCGGATCTTCGCGGGGA	502
Qy	ATGGGCTCTCGATGTAGATCT	203
Db	ATGGGCTCTCGATGTAGATCT	5049

US-09-991-209-25

APPLICANT: Dunn-Coleman, Nigel

**TITLE OF INVENTION:** Content and Digestibility of Plant Cell Walls by Targeted Enzymes

CURRENT FILING DATE: 2002-07-02  
PRIOR APPLICATION NUMBER: US 60/346 609

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; SOFTWARE: FastSEQ for Windows Version 4.0
CSCD ID NO 35
```

ORGANISM: Artificial Sequence

Query Match 44.78. 50

60 50 40 30 20 10 0

61 120

121 AAGGAGGGCAATCTTCACCGCCCTGCACCTCAGGAGGACGAATCTTGTGCGGGA 180

[illegible]

RESULT 14  
US-09-991-209-38  
; Sequence 38, Application US/09991209  
; Publication No. US2003024009A1  
; GENERAL INFORMATION:  
; APPLICANT: Dunn-Coleman, Nigel  
; APPLICANT: Langdon, Timothy  
; APPLICANT: Morse, Phillip  
; TITLE OF INVENTION: Manipulation of the Phenolic Acid  
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted



```

/ TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
/
/ FILE REFERENCE: CG648-2
/
/ CURRENT APPLICATION NUMBER: US/09/991,209
/
/ CURRENT FILING DATE: 2002-07-02
/
/ PRIOR APPLICATION NUMBER: US 60/249,608
/
/ PRIOR FILING DATE: 2000-11-17
/
/ NUMBER OF SEQ. ID NOS: 97
/
/ SOFTWARE: FastSeq for Windows Version 4.0
/
/ SEQ ID NO 38
/
/ LENGTH: 5295
/
/ TYPE: DNA
/
/ ORGANISM: Artificial Sequence
/
/ FEATURE:
/
/ OTHER INFORMATION: pUG4 vector
/
/ US-09-991-209-38

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Query Match	44.7%;	Score 203;	DB 10;	Length 5295;
Best Local Similarity	100.0%;	Pred. No. 5.6e-94;		
Matches 203; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

61 CTTTGCCCTGTGATGTTGGGTGGGCGAAGCGGCTTCGTGCGCCAGATCGGTCCGCGG 120  
5041 CTTTGGCCCTGTGATGTTGGGTGGGCGAAGCGGCTTCGTGCGCCAGATCGGTCCGCGG 51000

0y 121 AGGGGCGGGATCTCGCGCGTCCTCCGGGCGTGAAGTCGCGCCGGATCTCCGGGGA 180  
 Db 5101 AGGGGCGGGATCTCGCGCGTCCTCCGGGCGTGAAGTCGCGCCGGATCTCCGGGGA 5160

[illegible]

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RESULT 15
US-09-991-209-27
; Sequence 27, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; FILE REFERENCE: GCG48-2
; FILE REFERENCE: Expression of Genes Encoding Cell Wall Degrading Enzymes
; CURRENT APPLICATION NUMBER: US/09/991,209
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 5327
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pTP4a2 vector
US-09-991-209-27

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Query Match	44.7%;	Score 203;	DB 10;	length 5327;
Best Local Similarity	100.0%;	Pred. No. 5.6e-94;		
Matches 203; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

61 CTTTGGCCTTGGTAGTTGGGTCGACAGCGCGCTTCGTCCGCCAGATCGGTGCGCGG 120

Accession	Sequence	Length
D8	CTTTGGCCTTGTAGTTGTGGGTGGGACAGACGGCTTCGTGCGCCAAATCGATGATCGCGGG	4908
D8	4849	
OY	AGGGGCGGGGATCTTCGCGGGCTGGGGTCTCCGGGGCGTGAATCGGCCCGGATCTCGCGGGGA	180
OY	121	
D8	AGGGGCGGGGATCTTCGCGGGCTGGGGTCTTCGGGGCGTGAATCGGCCCGGATCTCGCGGGGA	4968
D8	4909	
OY	ATGGGGCTCTCGGATGTAGATCT	203
OY	181	
D8	ATGGGGCTCTCGGATGTAGATCT	4991
D8	4969	

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Job time : 242.829 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2005, 22:05:26 ; Search time 4919.01 Seconds  
(without alignments)  
15416.180 Million cell updates/sec

Title: US-10-758-799-3

Perfect score: 1565

Sequence: 1 GAATTCCTGCAGGTCAACG.....TTTTTGTAGTACGACG 1565

Scoring table: IDENTITY NJC

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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.\*

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2: gb\_Htg.\*

3: gb\_In.\*

4: gb\_Om.\*

5: gb\_Ov.\*

6: gb\_Pat.\*

7: gb\_Ph.\*

8: gb\_Pl.\*

9: gb\_Pr.\*

10: gb\_Ro.\*

11: gb\_Sts.\*

12: gb\_Sy.\*

13: gb\_Un.\*

14: gb\_Vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	1565	100.0	1565	6	BD128391
4	1021	65.2	1021	6	A94723
5	1021	65.2	1021	6	AR559743
6	1021	65.2	1021	6	BD128389
7	496.4	31.7	1264	8	MZEH3C4
8	458.2	29.3	4895	12	AY452735
9	454	29.0	454	6	AR559744
10	454	29.0	454	6	BD128390
11	428.8	27.4	1392	6	IS0114
12	428.8	27.4	1392	6	IS0115
13	428.8	27.4	1404	6	IS0115
14	428.8	27.4	2199	6	IS0113
15	426.2	27.2	623	6	AX467609
16	426.2	27.2	623	6	OSACT1
17	392	25.0	7943	6	AX093010
18	392	25.0	9143	6	AX093007
19	392	25.0	9143	6	AX093007

20	392	25.0	10003	6	AX093016	AX093016 Sequence
21	390.4	24.9	470	6	AX555357	AX555357 Sequence
22	384.8	24.6	9359	6	AX384394	AX384394 Sequence
23	384.8	24.6	9359	6	AX473364	AX473364 Sequence
24	378.4	24.2	4032	6	A71435	A71435 Sequence 5
25	378.4	24.2	4032	6	AR207453	AR207453 Sequence
26	378.4	24.2	4032	6	AR564463	AR564463 Sequence
27	378.4	24.2	4032	6	BD069509	BD069509 Improved
28	377.4	24.1	7545	6	AX840288	AX840288 Sequence
29	377.4	24.1	11643	6	AX840289	AX840289 Sequence
30	375.8	24.0	3039	6	AR271021	AR271021 Sequence
31	375.8	24.0	3039	6	AR271022	AR271022 Sequence
32	375.8	24.0	3044	6	AR271033	AR271033 Sequence
33	375.8	24.0	3450	6	AR271020	AR271020 Sequence
34	375.8	24.0	3455	6	AR271032	AR271032 Sequence
35	375.8	24.0	3469	6	AR271023	AR271023 Sequence
36	375.8	24.0	6865	6	AX093008	AX093008 Sequence
37	375.8	24.0	10003	6	AX093016	AX093016 Sequence
38	375.2	24.0	147344	8	AC091532	AC091532 Oryza sat
39	368.6	23.6	13485	12	AY225220	AY225220 Cloning v
40	368.4	23.5	13474	12	AY225219	AY225219 Cloning v
41	358.8	22.9	2378	6	AR229555	AR229555 Sequence
42	333.2	21.3	3694	6	AR174859	AR174859 Sequence
43	333.2	19.8	3877	6	AR174858	AR174858 Sequence
44	310.2	19.8	2107	6	AR229556	AR229556 Sequence
45	310.2	19.8	2122	6	AR229554	AR229554 Sequence

## ALIGNMENTS

RESULT 1	A94725	Sequence 3 from Patent WO9934005.	DNA	linear	PAT 26-JAN-2000
LOCUS	A94725	1565 bp			
DEFINITION	A94725				
ACCESSION	A94725				
VERSION	A94725.1	GI:6778990			
KEYWORDS					
SOURCE	unidentified				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 1565)				
AUTHORS	Derose, R. and Frey, S. et al.				
TITLE	MAIZE H3C4 PROMOTER ASSOCIATED WITH FIRST RICE ACTIN INTRON, CHIMERIC GENE CONTAINING IT AND TRANSFORMED PLANT				
JOURNAL	Patent: WO 9934005-A 3 08-JUL-1999;				
	RHONE POULENC AGROCHIMIE (FR)				
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	1102..1555				
ORIGIN					
	promoter				
	intron				
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Best Local Similarity	100.0%;	Pred. No. 0;			
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DB	1	GAATTCCTGCAGGTCAACGATCCCTTATGTCACCACTTACTGATGCAATTCAT	60		
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DB	61	TTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	120		
QY	121	TTCGCTCTCAACATTCATTCGCTCAAGTATGATGATGATGATGATGATGATGAT	180		
DB	121	TTCGCTCTCAACATTCATTCGCTCAAGTATGATGATGATGATGATGATGATGAT	180		
QY	181	TTCTTCATATATTTTTTCTTATACATATTTGGGCTTACATATTCATCATATATCA	240		

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RESULT 2  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
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REFERENCE  
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JOURNAL  
FEATURES  
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ORIGIN

Query Match 100.0%; Score 1565; DB 6; Length 1565;  
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ACCESSION A94723  
VERSION A94723.1 GI:6778988  
KEYWORDS  
SOURCE  
ORGANISM  
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unclassified.  
REFERENCE  
1 (bases 1 to 1021)  
AUTHORS  
Derose,R. and Freysstine,G.  
TITLE  
MAIZE H3C4 PROMOTER ASSOCIATED WITH FIRST RICE ACTIN INTRON,  
JOURNAL  
CHIMERIC GENE CONTAINING IT AND TRANSFORMED PLANT  
Patent: WO 9934005-A 1 08-JUL-1999;  
RHOBE POULENC AGROCHIMIE (PR)  
FEATURES  
source  
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Location/Qualifiers  
ORIGIN  
Promoter  
Query Match 65.2%; Score 1021; DB 6; Length 1021;  
Best Local Similarity 100.0%; Pred.No. 1.7e-208;  
Matches 1021; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Qy 387 CATTAATCATTTTATTTTACTTAAACGATTTTAAAGTATTCAAACGATGAAGAAC 446  
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387 CATTAATCATTTTATTTTACTTAAACGATTTTAAAGTATTCAAACGATGAAGAAC 446  
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QY 1047 G 1047  
Db 1021 G 1021

RESULT 5  
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LOCUS AR559743 1021 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 1 from patent US 6750378.  
ACCESSION AR559743  
VERSION AR559743.1 GI:53969841  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 1021)  
AUTHORS Derose R. and Freysinet G.  
TITLE Maize H3c4 promoter combined with the first intron of rice actin,  
chimeric gene comprising it and transformed plant  
JOURNAL Patent: US 6750378-A 1 15-JUN-2004;  
FEATURES  
source location/Qualifiers  
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Query Match 65.2%; Score 1021; DB 6; Length 1021;  
Best Local Similarity 100.0%; Pred. No. 1.7e-208;  
Matches 1021; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 CTTATGACACATTTACTGTAATGCAATCAATTAATTAATGAATGCAAACTTTCTAAT 86

Db 1 CTTATGACACATTTACTGTAATGCAATCAATTAATTAATGAATGCAAACTTTCTAAT 60  
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QY 1047 G 1047  
Db 1021 G 1021

RESULT 6

Db	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	source
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QY	627	GCGCCTCTCAATTTTCACTCGAGCGCCCAATTTTCAAGTTTTCACCCGAAGCGCCAGCC												
Db	601	GCGCCTCTCAATTTTCACTCGAGCGCCCAATTTTTCAGTTTTCACCGAAGCGCCAGCC												
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Db	781	GAACCAACCATCAACGCGGATCGTCCCTACGCTTTCACCTCATCGGCGCGCTCATCTCA												
QY	867	TCCAAACCTTATTCGTTACCTTGGCCCATCTCTCGAATAAATTTCTGGCTTCGGCTCCGC												
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QY	1047	G 1047												
Db	1021	G 1021												
RESULT 7														
MZEH3C4														
LOCUS	MZEH3C4	Maize (Zea mays) histone H3 gene (H3C4), complete cds.	1264 bp	DNA	linear	PLN 27-APR-1993								
DEFINITION	MZEH3C4	Maize (Zea mays) histone H3 gene (H3C4), complete cds.												
ACCESSION	M13379													
VERSION	M13379.1	GI:168496												
KEYWORDS	histone.													
SOURCE	Zea mays													
ORGANISM	Zea mays													
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	clade; Panicoideae; Andropogoneae; Zea.													
	1 (bases 1 to 1264)													
	Chaubet,N., Phillips,G., Chaboute,M.-E., Ehling,M. and Gigot,C.													
	Nucleotide sequences of two corn histone H3 genes. Genomic													
	organization of the corn histone H3 and H4 genes													
	Plant Mol. Biol. 6, 253-263 (1986)													
	Original source text: Maize DNA, clone H3C4.													
	Draft entry and printed copy of the sequence [1] kindly provided by													
	C.Gigot, 10-OCT-1986.													
	Location/Qualifiers													
	1..1264													



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 ORIGIN 54 bp upstream of BglII site.

Query Match 31.7%; Score 496.4; DB 8; Length 1264;  
 Best Local Similarity 95.9%; Pred. No. 6,7e-96;  
 Matches 520; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

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 QY 650 GCGCCACATTTTCACTGTTTACCGAAGCGCGCCGCTGCTAACCAAAATTTGTACG 709  
 DB 122 GCGCCACATTTTCACTGTTTACCGAAGCGCGCCGCTGCTAACCAAAATTTGTACG 181  
 QY 710 GTGACGCGGTTTCAAAAGATCGGAAACCATCTGACCCAGACTAGTAGGCGCTCG 769  
 DB 182 GTGACGCGGTTTCAAAAGATCGGAAACCATCTGACCCAGACTAGTAGGCGCTCG 241  
 QY 770 GATCTCTCTGATTAGTCTTACCAATAGAGCCGCAACCAATCAAGCGGATCGT 829  
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 DB 302 CCTTACGCTTCACTATGCGCGCGCTGCTCATCTCCATCAACCACTTATTCCTT 361  
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 QY 950 TCAAGAGCATGCGATCATGCGCAATCCCGCAAAATCAACACTCCCAATTCACGCG 1009  
 DB 422 TCAAGAGCATGCGATCATGCGCAATCCCGCAAAATCAACACTCCCAATTCACGCG 481  
 QY 1010 TCGCCACCAACTCGCGCTCTCGCGCGCAAGCAACCAAGAAATGCGCGCAAGCGGCTG 1069  
 DB 482 TCGCCACCAACTCGCGCTCTCGCGCGCAAGCAACCAAGAAATGCGCGCAAGCGGCTG 541  
 QY 1070 AG 1071  
 DB 542 AG 543

RESULT 8  
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 LOCUS Reporter vector pACTXN, complete sequence.  
 DEFINITION AY452735  
 ACCESSION AY452735  
 VERSION AY452735.1 GI:39636979  
 KEYWORDS Reporter vector pACTXN  
 SOURCE Reporter vector pACTXN  
 ORGANISM Other sequences; artificial sequences; vectors.  
 REFERENCE 1 (bases 1 to 4895)  
 Vickers, C.E., Xue, G.P. and Greshoff, P.M.  
 TITLE A synthetic xylanase as a novel reporter in plants  
 JOURNAL Plant Cell Rep. 22 (2), 135-140 (2003)  
 MEDLINE 22867549  
 PUBMED 12845475  
 REFERENCE 2 (bases 1 to 4895)  
 Vickers, C.E.  
 TITLE Direct Submission  
 JOURNAL Submitted (29-OCT-2003) ARC Centre for Integrative Legume Research,  
 The University of Queensland, Room 213, John Hines Building (69),  
 St. Lucia, QLD 4072, Australia

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 3339..3792 /note="intron 1 from rice actin gene; Act1"  
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 4895 /note="SP6 RNA polymerase transcription initiation site"  
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 Best Local Similarity 88.7%; Pred. No. 1.2e-87;  
 Matches 542; Conservative 0; Mismatches 63; Indels 6; Gaps 4;

QY 958 CATGCGATCATGCGCAATCCCCAGAAATCAACACTCCCAATTCACGCTGCCACCA 1017  
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 QY 1018 ACTGCGGCTCTTCGCGCAAGCAACCAAGAAATGCGCGCAAGCGGCTGAGCTTCCT 1077  
 DB 3255 ACCCTACCAACACCAACACACACACTCTCCCCCTGCTGCGGACGACGAGCTCTTC 3314  
 QY 1078 CCCCCCTCCCTCCGCGCGCGCGGTAACACCCGCGCTCTCTCTTCTTCTCGCT 1137  
 DB 3315 CCCCCCTCCCTCCGCGCGCGCGGTAACACCCGCGCTCTCTCTTCTTCTCGCT 3374  
 QY 1138 TTTTCTTCTGCTCGGCTCGATCTTGGCTTGGTAGTTGGTGGGCGAGAGCGGCT 1197  
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 QY 1258 AGTGGCCCGGATCTCGCGGGAATGAGGCTCTCGAGATGATGATCT--GATCCGCGCTT 1315  
 DB 3495 AGTGGCCCGGATCTCGCGGGAATGAGGCTCTCGAGATGATGATGATGATGATGATGAT 3554



VERSION	BD128390.1	GI:23223335
KEYWORDS	JP 2002500016-A/2.	
SOURCE	unidentified	
ORGANISM	unclassified.	
REFERENCE	1 (bases 1 to 454)	
AUTHORS	Durose,R. and Freysaier,G.	
TITLE	Corn H3C4 promoter bonded to the first intron of rice actin,	
JOURNAL	chimeric gene containing this promoter and transgenic plant Patent: JP 2002500016-A 2 08-JAN-2002;	
COMMENT	AVENTIS CROPS SCIENCE SA OS Unidentified PN JP 2002500016-A/2 PD 08-JAN-2002 PF 22-DEC-1998 JP 2000526660 PI RICHARD DUROSE, GEORGES FREYSAIER PC C12N15/09,A01H5/00,C07K14/21,C07K14/415,C07K19/00,C12N5/10, PC C1201/68, PC C12N15/00,C12N5/00 CC Strandedness: Single; CC Topology: Linear; CC Corn H3C4 promoter bonded to the first intron of rice actin, CC chimeric gene CC containing this promoter and transgenic plant FH Key FT source FT location/Qualifiers 1. .454 /organism='Unidentified'. location/Qualifiers 1. .454 /organism='unidentified' /mol_type='Genomic DNA' /db_xref='taxon:32644'	
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Best Local Similarity	100.0%; Pred. NO. 7.6e-87;	
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OY	1162 CTTCGGCTTGTAAGTTGGTGGGCGAGACCGGCTTCGTGCGCCAATCGATGCGCGG	1221
Db	61 CTTCGGCTTGTAAGTTGGTGGGCGAGACCGGCTTCGTGCGCCAATCGATGCGCGG	120
OY	1222 AGGGCGGGGATCTCGCGGCTGGCGCTCCGGGCGTAGATCGGCCCGCATCTTCGCGGGGA	1281
Db	121 AGGGCGGGGATCTCGCGGCTGGCGCTCCGGGCGTAGATCGGCCCGCATCTTCGCGGGGA	180
OY	1282 ATGGGGCTCTCGGATGTAGATCTGATCCGCGCTGTTGGGGGAGAATGATGGGCGATTAA	1341
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OY	1402 TATATATTTCTGCTCTGCTGTCAAGGCTTAGATGATGCTTATGTTTCTTTT	1461
Db	301 TATATATTTCTGCTCTGCTGTCAAGGCTTAGATGATGCTTATGTTTCTTTT	360
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DEFINITION	IS0114	Sequence 6 from patent US 5641876.				
ACCESSION	IS0114					
VERSION	IS0114.1	GI:2472334				
KEYWORDS	.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	Unclassified.					
AUTHORS	1 (bases 1 to 1392)					
TITLE	McElroy,D. and Wu,R.					
JOURNAL	Rice actin gene and promoter					
FEATURES	Parent: US 5641876-A 6 24-JUN-1997;					
SOURCE	Location/Qualifiers					
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Best Local Similarity	84.9%; Pred.No. 2.2e-81;					
Matches 518; Conservative	0; Mismatches 82; Indels 10; Gaps 3;					
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OY	1018 ACTGCGCGTCTCTCGCGCGCAAGCAACAAAGGAATTTGACCGGCAACCGCGGTGAG	1077				
DB	835 ACCGTAC	894				
OY	1078 CCCCCCTCCCCCTCGCGCGCGCGCGGTAAACACACCCCGC--CCCTCTCTCTTTCTTTC	1135				
DB	895 CCCCCCTCCCCCTCGCGCGCGCGCGGTAAACACACCCCGGTCCCTCTCTTTCTTTC	954				
OY	1136 GTTTTTTTTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1195				
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OY	1196 CTTCGTGCGCCAGATCGGTGCGCGGAGGCGGAGATCTCGCGGCTGCGGTCTCCGAG	1255				
DB	1014 CTTCGTGCGCCAGATCGGTGCGCGGAGGCGGAGATCTCGCGGCTGCGGTCTC	1066				
OY	1256 TGAATCGCCCGGATCTCTCGCGGGAATGCGGCTCTCGATGATGATCTGATCCGCG	1315				
DB	1067 GGCGTGGCGCGGATCTCTCGCGGGAATGCGGCTCTCGATGATGATCTGATCCGCG	1126				
OY	1316 GTTCGGGGAGATGATGCGGCGCTTAATTTTCCGATGCTAAACAAGTCAAGAAAGG	1375				
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OY	1436 GTGCTAGAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1495				
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DEFINITION	Sequence 7 from patent US 5641876.					
ACCESSION	IS0115					

VERSION 150115.1 GI:2472335  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1404)  
AUTHORS McElroy, D. and Wu, R.  
TITLE Rice actin gene and promoter  
JOURNAL Patent: US 5641876-A 7 24-JUN-1997;  
FEATURES  
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Query Match 27.4%; Score 428.8; DB 6; Length 1404;  
Best Local Similarity 84.9%; Pred. No. 2.2e-81;  
Matches 518; Conservative 0; Mismatches 82; Indels 10; Gaps 3;  
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QY 1078 CCCCCCTCCCTCCGCGCGCGCGGTAAACACCCCG--CCCTCTCTCTTTCTTCTC 1135  
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DB 1024 CTTCGTGCGCCAGATCGGTGCGGCGGAGCGGAGCTTCGCGGCTG-----GTCTC 1076  
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QY 1556 GTAGACCATG 1565  
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RESULT 14  
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LOCUS Sequence 5 from patent US 5641876.  
DEFINITION  
ACCESSION 150113  
VERSION 150113.1 GI:2472333  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

Unclassified.  
REFERENCE 1 (bases 1 to 2199)  
AUTHORS McElroy, D. and Wu, R.  
TITLE Rice actin gene and promoter  
JOURNAL Patent: US 5641876-A 5 24-JUN-1997;  
FEATURES  
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ORIGIN  
Query Match 27.4%; Score 428.8; DB 6; Length 2199;  
Best Local Similarity 84.9%; Pred. No. 2.3e-81;  
Matches 518; Conservative 0; Mismatches 82; Indels 10; Gaps 3;  
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DB 1582 CAAAGAAAGCGCCCGCATCGCCACTATATACATACCCCGCTCTCTCCATCCCCCA 1641  
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DB 1642 ACCCTACACACACACACACACCTCTCCCGCTGCGCGAGACGAGCTCTC 1701  
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QY 1316 GTTGGGGGAGATGATGGGCGGTTTAAATTTCGCATGTAAACAAGATCAGGAGAGG 1375  
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QY 1376 GAAAAGGCACTATGTTTATTTTATTTTATTTCTGCTGCTGCTCAGGCTTAGAT 1435  
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DB 2114 CGGTAGTTTCTTTTCATGATTTTGACAATGACAGCTCGTGGGAGCTTTTGTAG 2173  
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RESULT 15  
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LOCUS Sequence 4 from patent US 5641876.  
DEFINITION  
ACCESSION 150112  
VERSION 150112.1 GI:2472332  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 5643)  
AUTHORS McElroy, D. and Wu, R.  
TITLE Rice actin gene and promoter

JOURNAL Patent: US 5641876-A 4 24-JUN-1997;  
FEATURES Location/Qualifiers  
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Query Match 27.4%; Score 428.8; DB 6; Length 5643;

Best Local Similarity 84.9%; Pred. No. 2.6e-81;

Matches 518; Conservative 0; Mismatches 82; Indels 10; Gaps 3;

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QY 1078 CCCCCCTCCCTCGCGCGCGCGGTAAACACCCCGC--CCCTCTCTCTTCTTCTCC 1135
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Db 2117 CGGAGTTTCTTCTTCTTCTTCTTGGGTAGAAATTTGAATCCTCAGCATTTTCTAG 2176
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Minimum DB seq length: 0

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4: Geneseq20018:\*  
5: Geneseq20018:\*  
6: Geneseq20028:\*  
7: Geneseq20028:\*  
8: Geneseq20038:\*  
9: Geneseq20038:\*  
10: Geneseq20038:\*  
11: Geneseq20048:\*  
12: Geneseq20048:\*  
13: Geneseq20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1565	100.0	1565	2	AAZ91039 Chimeric
2	1021	65.2	1021	2	AAZ91037 Maize his
3	454	29.0	454	2	AAZ91038 Rice acti
4	445.6	28.5	13680	12	ADP73931 Plasmid P
5	428.8	27.4	1392	2	AAT80053 Rice acti
6	428.8	27.4	2199	2	AAT80052 Rice acti
7	428.8	27.4	5643	2	AAT80055 Rice acti
8	426.2	27.2	623	3	AAZ47117 Rice acti
9	426.2	27.2	623	6	ABK86738 Rice acti
10	392	25.0	7943	4	AAF80289 Nucleotid
11	392	25.0	9143	4	AAF80286 Nucleotid
12	392	25.0	10003	4	AAF80295 Nucleotid
13	390.4	24.9	470	6	ABT07357 Reporcer
14	380.4	24.9	470	10	ADP49181 Rice acti
15	384.8	24.6	9359	6	ABK11039 pVDH636 v
16	384.8	24.6	9359	6	ABK10687 Transform
17	378.4	24.2	4032	2	AAV23237 Plasmid P
18	377.4	24.1	5118	12	ADP73930 Plasmid P
19	377.4	24.1	7545	10	ACF58343 Nucleotid
20	377.4	24.1	11643	10	ACF58344 Nucleotid

## ALIGNMENTS

21	375.8	24.0	491	3	AAZ51179	AAZ51179	Intron of
22	375.8	24.0	491	8	ACA05324	ACA05324	Rice acti
23	375.8	24.0	3039	3	AAZ51644	AAZ51644	Bacillus
24	375.8	24.0	3039	3	AAZ51645	AAZ51645	Bacillus
25	375.8	24.0	3039	10	AAZ51645	AAZ51645	Bacillus
26	375.8	24.0	3039	10	AAZ51645	AAZ51645	Bacillus
27	375.8	24.0	3039	10	AAZ51645	AAZ51645	Bacillus
28	375.8	24.0	3039	10	AAZ51645	AAZ51645	Bacillus
29	375.8	24.0	3044	3	AAZ51656	AAZ51656	Bacillus
30	375.8	24.0	3044	10	AAZ51656	AAZ51656	Bacillus
31	375.8	24.0	3044	10	AAZ51656	AAZ51656	Bacillus
32	375.8	24.0	3450	3	AAZ51643	AAZ51643	Bacillus
33	375.8	24.0	3450	10	AAZ51643	AAZ51643	Bacillus
34	375.8	24.0	3450	10	AAZ51643	AAZ51643	Bacillus
35	375.8	24.0	3455	3	AAZ51655	AAZ51655	Bacillus
36	375.8	24.0	3455	10	AAZ51655	AAZ51655	Bacillus
37	375.8	24.0	3455	10	AAZ51655	AAZ51655	Bacillus
38	375.8	24.0	3469	3	AAZ51646	AAZ51646	Bacillus
39	375.8	24.0	3469	10	AAZ51646	AAZ51646	Bacillus
40	375.8	24.0	3469	10	AAZ51646	AAZ51646	Bacillus
41	375.8	24.0	5170	12	ADK98488	ADK98488	B. thuring
42	375.8	24.0	5600	12	ADK98490	ADK98490	B. thuring
43	375.8	24.0	6865	4	AAF80287	AAF80287	Nucleotid
44	375.8	24.0	10003	4	AAF80295	AAF80295	Nucleotid
45	366.4	23.4	2181	10	ADC84543	ADC84543	Rice acti

## RESULT 1

AAZ91039 standard; DNA; 1565 BP.

AC	AAZ91039;						
XX							
DT	17-OCT-2003	(revised)					
DT	06-JUN-2000	(first entry)					
XX							
DE	Chimeric maize H3C4 promoter/rice actin gene intron 1 regulatory region.						
XX							
KW	Regulatory element; monocotyledonous vegetable plant cell; maize;						
KW	histone H3C4; promoter; rice actin gene intron; chimeric; ss;						
XX	herbicide resistance.						
OS	Zea mays.						
OS	Oryza sativa.						
OS	Chimeric.						
XX							
PN	FR2772787-AL.						
XX							
PD	25-JUN-1999.						
XX							
PF	24-DEC-1997;	97PR-00016726.					
XX							
PR	24-DEC-1997;	97PR-00016726.					
XX							
PA	(RHON ) RHONE-BOULENC AGROCHIMIE.						
XX							
PI	Derose R, Freysinet G;						
XX							
DR	WPI; 1999-397352/34.						
PT	5' chimeric regulatory region comprising maize histone H3C4 promoter and						
PT	rice actin gene first intron.						
XX							
PS	Claim 8; Page 15-16; 24pp; French.						
XX							
CC	The invention relates to a DNA sequence comprising a 5' regulatory						
CC	element for the expression of a heterologous gene in a monocotyledonous						
CC	vegetable plant cell. The DNA (this sequence) comprises: (a) a functional						
CC	fragment of the maize histone H3C4 promoter sequence (AAZ91037; and (b) a						
CC	functional fragment of the first intron of the rice actin gene						

CC (AAZ91038). The chimeric regulatory region is useful for the expression  
CC of heterologous genes that confer resistance to certain herbicides, or  
CC that have novel agronomical properties in monocotyledons. In particular,  
CC the chimeric 5' regulatory gene is linked to an enzyme that confers  
CC resistance to a specific herbicide. This is useful for controlling weeds  
CC in fields of plants/grains that have been transformed with the chimeric  
CC gene. The herbicide can be applied to the field without affecting the  
CC plant/grain. (Updated on 17-OCT-2003 to standardise OS field)



PR 24-DEC-1997; 97FR-00016726.  
 XX (RHON ) RHONE-POULENC AGROCHIMIE.  
 XX Derose R. Freyssinet G;  
 XX WPI; 1999-397352/34.  
 DR  
 XX  
 PT 5' chimeric regulatory region comprising maize histone H3C4 promoter and  
 PT rice actin gene first intron.  
 XX  
 PS Claim 3; Page 13; 24pp; French.  
 XX  
 CC The invention relates to a DNA sequence (AA291039) comprising a 5'  
 CC regulatory element for the expression of a heterologous gene in a  
 CC monocotyledonous vegetable plant cell. The DNA comprises: (a) a  
 CC functional fragment of the maize histone H3C4 promoter sequence (this  
 CC sequence); and (b) a functional fragment of the first intron of the rice  
 CC actin gene (AA291038). The chimeric regulatory region is useful for the  
 CC expression of heterologous genes that confer resistance to certain  
 CC herbicides, or that have novel agronomical properties in monocotyledons.  
 CC In particular, the chimeric 5' regulatory gene is linked to an enzyme  
 CC that confers resistance to a specific herbicide. This is useful for  
 CC controlling weeds in fields of plants/grains that have been transformed  
 CC with the chimeric gene. The herbicide can be applied to the field without  
 CC affecting the plant/grain  
 CC  
 XX  
 SQ Sequence 1021 BP; 283 A; 275 C; 140 G; 323 T; 0 U; 0 Other;  
 Query Match 65.2%; Score 1021; DB 2; Length 1021;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-232;  
 Matches 1021; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 CTTATGACCACTTACTGTAATGCAATCAATTAATGAATAGCAACTTTTCTATT 86  
 DB 1 CTTATGACCACTTACTGTAATGCAATCAATTAATGAATAGCAACTTTTCTATT 60  
 QY 87 ACTTCTTTACTAATCAATATCTGTTTAAATTCAGTCCCTCAACTTCTGCTCAAG 146  
 DB 61 ACTTCTTTACTAATCAATATCTGTTTAAATTCAGTCCCTCAACTTCTGCTCAAG 120  
 QY 147 TATAGTGAGAGCTGCAAAATTTACTATTTTCTTCATATTTTCTTCCTATACA 206  
 DB 121 TATAGTGAGAGCTGCAAAATTTACTATTTTCTTCATATTTTCTTCCTATACA 180  
 QY 207 CATTGTTGGCTTACATCAATCATATATCCATCTTCCGCTGCTCTCAAAAGATT 266  
 DB 181 CATTGTTGGCTTACATCAATCATATATCCATCTTCCGCTGCTCTCAAAAGATT 240  
 QY 267 CCATCTCTGTAATCTTATCTCTCCAAATACGTTCTTAATCAGGCTCTTAAGCAA 326  
 DB 241 CCATCTCTGTAATCTTATCTCTCCAAATACGTTCTTAATCAGGCTCTTAAGCAA 300  
 QY 327 TACCTAATATAGAGACATTTTATTTTGTACATCAATTTGTCAATCTCTCAAAAG 386  
 DB 301 TACCTAATATAGAGACATTTTATTTTGTACATCAATTTGTCAATCTCTCAAAAG 360  
 QY 387 CATTATACATATTTAGTTTACTAAACCGATTTATTAAGTATTTCAACGATGAAGAC 446  
 DB 361 CATTATACATATTTAGTTTACTAAACCGATTTATTAAGTATTTCAACGATGAAGAC 420  
 QY 447 TGTATAGATAATTTCTATATATAGAGATCCAGTAGCGTTCTTAATTTAGATATAT 506  
 DB 421 TGTATAGATAATTTCTATATATAGAGATCCAGTAGCGTTCTTAATTTAGATATAT 480  
 QY 507 TTAGAGAGCGCTGTGAAGAAACGTAAGAAATCTTTGATATTTATTTAGGATGAGT 566  
 DB 481 TTAGAGAGCGCTGTGAAGAAACGTAAGAAATCTTTGATATTTATTTAGGATGAGT 540  
 QY 567 AGCCTTATAGCTTTATAGATCTTTGTGAGACCGACGCTTATACCGGTTATTTTCGCGATT 626  
 DB 541 AGCCTTATAGCTTTATAGATCTTTGTGAGACCGACGCTTATACCGGTTATTTTCGCGATT 600

QY 627 GGCCCTCTGATTTTCACTCCAGCGCCCAATTTTCAAGTTTTACCGAAGCGCCAGCC 686  
 DB 601 GGCCCTCTGATTTTCACTCCAGCGCCCAATTTTCAAGTTTTACCGAAGCGCCAGCC 660  
 QY 687 TGCCTAACCAACAAATTTGGTACGGTGCAGCGGTTTCAAAAGAGTCGAAACCATCTGC 746  
 DB 661 TGCCTAACCAACAAATTTGGTACGGTGCAGCGGTTTCAAAAGAGTCGAAACCATCTGC 720  
 QY 747 ACCCAGCGACTAGTAGGCGCTCGGATCTCTCGATTAAGTCTTACGCAATAGAGCCCA 806  
 DB 721 ACCCAGCGACTAGTAGGCGCTCGGATCTCTCGATTAAGTCTTACGCAATAGAGCCCA 780  
 QY 807 GAACCAACCATCAACGAGATTCGCTTACGCTTCACTCATCGGCGGCTCCATCTCCA 866  
 DB 781 GAACCAACCATCAACGAGATTCGCTTACGCTTCACTCATCGGCGGCTCCATCTCCA 840  
 QY 867 TCCCAACCTATTCCTGTACTCTTCCCATCTTCCGAAAAATTTCTGCGTCTCCGCG 926  
 DB 841 TCCCAACCTATTCCTGTACTCTTCCCATCTTCCGAAAAATTTCTGCGTCTCCGCG 900  
 QY 927 ACCTACTAACAATATCCATCCATCCATCAACGACATCGCATCTGCCAAATCCCGAGAAA 986  
 DB 901 ACCTACTAACAATATCCATCCATCCATCAACGACATCGCATCTGCCAAATCCCGAGAAA 960  
 QY 987 ATCAACACTCCCAATTTCCAGCTGCCAACCACTGCGGCTCTCCGCGCAACGACCAAA 1046  
 DB 961 ATCAACACTCCCAATTTCCAGCTGCCAACCACTGCGGCTCTCCGCGCAACGACCAAA 1020  
 QY 1047 G 1047  
 DB 1021 G 1021

RESULT 3  
 AA291038  
 ID AA291038 standard; DNA; 454 BP.  
 XX  
 AC AA291038;  
 DT 06-JUN-2000 (first entry)  
 XX  
 DE Rice actin gene intron 1 sequence.  
 XX  
 KW Regulatory element; monocotyledonous vegetable plant cell; maize;  
 KW histone H3C4; promoter; rice actin gene intron; chimeric; ss;  
 KW herbicide resistance.  
 XX  
 OS Oryza sativa.  
 XX  
 PN FR272787-A1.  
 XX  
 PD 25-JUN-1999.  
 XX  
 PF 24-DEC-1997; 97FR-00016726.  
 XX  
 PR 24-DEC-1997; 97FR-00016726.  
 XX  
 XX (RHON ) RHONE-POULENC AGROCHIMIE.  
 XX PA  
 XX Derose R. Freyssinet G;  
 XX PI  
 XX WPI; 1999-397352/34.  
 DR  
 XX  
 PT 5' chimeric regulatory region comprising maize histone H3C4 promoter and  
 PT rice actin gene first intron.  
 XX  
 PS Claim 5; Page 14; 24pp; French.  
 XX  
 CC The invention relates to a DNA sequence (AA291039) comprising a 5'  
 CC regulatory element for the expression of a heterologous gene in a  
 CC monocotyledonous vegetable plant cell. The DNA comprises: (a) a  
 CC functional fragment of the maize histone H3C4 promoter sequence  
 CC (AA291037); and (b) a functional fragment of the first intron of the rice







ID	Accession	Gene Name	Species	Length (bp)	GC Content (%)	GC Skew (%)	GC Bias (%)	GC Bias (2-mer)	GC Bias (3-mer)	GC Bias (4-mer)	GC Bias (5-mer)	GC Bias (6-mer)	GC Bias (7-mer)	GC Bias (8-mer)	GC Bias (9-mer)	GC Bias (10-mer)	GC Bias (11-mer)	GC Bias (12-mer)	GC Bias (13-mer)	GC Bias (14-mer)	GC Bias (15-mer)	GC Bias (16-mer)	GC Bias (17-mer)	GC Bias (18-mer)	GC Bias (19-mer)	GC Bias (20-mer)
XX	AA780055	standard; cDNA, 5643 BP.																								
XX	AA780055																									
AC	AA780055																									
DT	25-MAR-2003	(revised)																								
DT	04-NOV-1997	(first entry)																								
XX		Rice actin 1 gene.																								
XX		Promoter; rice; actin 1 gene; cytoplasm; cytoskeleton; extension growth;																								
KW		cytoplasmic streaming; cell division; Rac1; maize; Adh1 promoter; ss.																								
OS		Oryza sativa.																								
PN		US5641876-A.																								
PD		24-JUN-1997.																								
XX		27-OCT-1993;																								
PF		93US-00144602.																								
XX		05-JAN-1990;																								
PR		90US-00461490.																								
PR		18-SEP-1991;																								
XX		91US-00762680.																								
PA		(CORR ) CORNELL RES FOUND INC.																								
XX																										
PI		Mu R, Mcelroy D;																								
XX																										
DR		WPI, 1997-340996/31.																								
PT																										
PT		Nucleic acid containing the promoter of the rice actin-1 gene - used to																								
XX		direct efficient expression of foreign genes in rice.																								

DB	Accession	Gene	Location/Qualifiers
DB	1765	GTGTTTTTTTTTCCGCTTCGCTTCGATCTTTGGCCTTGGTAATTTGGGGGCGAAG-GCGG	1823
QY	1196	CTTCGTCGCCAGATCGGTGCGCGGAGGGCGGAGATCTCGCGGCTGGCGTCTCCGGGCG	1255
DB	1824	CTTCGTCGCCAGATCGGTGCGCGGAGGGCGGAGATCTCGCGGCTGG-----GTCTC	1876
QY	1256	TGATTCGCGCCCGGATCTCTCGCGGGGAATGGGGCTCTCGGATGTGATCTGATCCGCCGT	1315
DB	1877	GGCGTGGCGCGCGGATCTCTCGCGGGGAATGGGGCTCTCGGATGTGATCTGATCCGCCGT	1936
QY	1316	GTTCGGGGGAGATGATGGGGCGTTTAAATTTCCGCATCTCTAAACAAGATCAGAAAGAGG	1375
DB	1937	GTTCGGGGGAGATGATGGGGCGTTTAAATTTCCGCATCTCTAAACAAGATCAGAAAGAGG	1998
QY	1376	GAAGAGGCACTATGTTTATATTTTATATATTTCTGCTGCTGCTGCTGCTGCTGCTGAT	1438
DB	1997	GAAGAGGCACTATGTTTATATTTTATATATTTCTGCTGCTGCTGCTGCTGCTGCTGAT	2056
QY	1436	GTGCTAGATCTTTCTTTCTTTTGTGGGTAGAAATTTGAATCCCTCAGATTTGTCAT	1495
DB	2057	GTGCTAGATCTTTCTTTCTTTTGTGGGTAGAAATTTGAATCCCTCAGATTTGTCAT	2116
QY	1496	CGGTAGTTTTCTTTATATGATTTGTACAATGACAGCTGCGGAGCTTTTGTGAT	1555
DB	2117	CGGTAGTTTTCTTTATATGATTTGTACAATGACAGCTGCGGAGCTTTTGTGAT	2176
QY	1556	GTAGACCATG 1565	
DB	2177	GTAGACCATG 2186	
RESULT 8			
AAZ47117			
ID	AAZ47117	standard; DNA; 623 BP.	
AC	AAZ47117;		
XX	15-MAR-2000	(first entry)	
DE	Rice Act1-GUS fusion gene 5' transcribed region.		
XX	Transformation; transgenic plant; pineapple; totipotent body; resistance;		
KM	pest; disease; maize; sucrose phosphate synthase; enzyme; sweetness;		
KM	chaumatin; antisense; inhibition; gene expression; ACC synthase; actin;		
KM	fruit ripening; polyphenol oxidase; browning reaction; chilling injury;		
KM	rice; beta-glucuronidase; ss.		
XX	Synthetic.		
OS	Key		
XX	TATA_signal		
FX	exon		
FT	misc_RNA		
FT	intron		
FT	exon		
FT	CDS		
FT	WT		
FT	PN		
XX	MO9958644-A1.		
XX	18-NOV-1999.		
XX	13-MAY-1999;		
PF	99WO-USO10576.		

```
XX 14-MAY-1998; 98US-00078862.
PR (UTMA-) UNIV HAWAII.
PA Nan G, Nagai C;
XX WPI; 2000-062292/05.
DR P-PSDB; AAY56018.
XX Stably transformed transgenic pineapple-like totipotent body and plants,
PT methods of transformation and culture.
XX Example 2; Fig 3; 87pp; English.
XX The invention relates to the generation of a stably transformed
CC transgenic pineapple-like totipotent body. The methods are used for the
CC production of transgenic pineapple-like totipotent bodies, and in
CC particular, transgenic plants derived from them. The plants can be
CC engineered to exhibit resistance to pests and disease and to exhibit
CC improved qualities. The transgenic bodies can be transformed with
CC constructs containing genes of interest as the maize sucrose phosphate
CC synthase enzyme (Genbank accession m97550) or a sweetness protein (e.g.
CC chaumatin) to increase the sweetness of the fruit. Alternatively,
CC constructs can include antisense sequences to inhibit gene expression,
CC e.g. an antisense construct to ACC synthase, which would delay fruit
CC ripening or to polyphenol oxidase (Genbank accession s40548) which would
CC prevent the browning reaction occurs during chilling injury. The
CC expression constructs comprises promoter which drives the expression of
CC the gene of interest. This sequence represents an example of a construct
CC and comprises the 5' transcribed region of the rice actin-1 gene linked
CC to the beta-glucuronidase enzyme coding sequence
XX
SQ Sequence 623 BP; 98 A; 184 C; 164 G; 177 T; 0 U; 0 Other;
Query Match 27.2%; Score 426.2; DB 3; Length 623;
Best Local Similarity 87.3%; Pred. No. 3.4e-91;
Matches 504; Conservative 0; Mismatches 63; Indels 10; Gaps 3;
QY 991 ACACCTCCCAATTCACGCTGCGACCACTGCGGCTCTCCGCGCAAGCAACCAAGGAA 1050
DB 10 ACCCCCCCTCTCTCCATCCGCCCAACCTTACCAACACACACACCTCTCTCC 69
QY 1051 TTGGCCGCCACCGCGGTGAGTCTCTCCCTCCCTCCGCGCGCGCGCGGTACACCC 1110
DB 70 CCTCTGCTGCGGACGACGAGCTCTCTCCCTCCCTCCGCGCGCGCGCGGTACACCC 129
QY 1111 CCGC--CCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1168
DB 130 CCGCGTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 189
QY 1169 CTGTGTAGTGGTGGGCGAGAGCGGCTTCTGTCGCCAGATCGTGGCGGAGGCGG 1228
DB 190 CTGTGTAGTGGTGGGCGAGAG--GCGGCTTCTGTCGCCAGATCGTGGCGGAGGCGG 248
QY 1229 GGAATCGGCGGCGGTGTCGCGGCGGTGAGTGGCGCGGATCTCTGCGGCGGAAATGGGCG 1288
DB 249 GGAATCGGCGGCGGTGTCGCGGCGGTGAGTGGCGCGGATCTCTGCGGCGGAAATGGGCG 301
QY 1289 TCTCGGATGTAGTGTGATCCGCGGTGTTGTTGGGCGAGATGATGATGATGATGATG 1348
DB 302 TCTCGGATGTAGTGTGATCCGCGGTGTTGTTGGGCGAGATGATGATGATGATGATG 361
QY 1349 CCAATGCTAAACAAGATCAGAGAGAGGAGAAAGGCGCATGTGTTATATTTTATATAT 1408
DB 362 CCAATGCTAAACAAGATCAGAGAGAGGAGAAAGGCGCATGTGTTATATTTTATATAT 421
QY 1409 TTCTGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1468
DB 422 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 481
QY 1469 GAATTTGAATCCCTCAGCATTTGTCATCGGTAGTTTCTTTTCATGATTTTGACAAAT 1528
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DB 482 GAATTTGAATCCCTCAGCATTTGTCATCGGTAGTTTCTTTTCATGATTTTGACAAAT 541
QY 1529 GCAGCTGTGTGCGGAGCTTTTGTAGGTAGCCATG 1565
DB 542 GCAGCTGTGTGCGGAGCTTTTGTAGGTAGCAATG 578
RESULT 9
ABK86738
ID ABK86738 standard; DNA; 623 BP.
XX
XX ABK86738;
XX
XX 24-SEP-2002 (first entry)
XX
XX Rice Act1 gene.
XX
XX Rice; gene; db; transgenic; plant; lignocellulose; cellulase; ligninase;
XX fermentable sugar; ethanol; fermentation; silage; feed; fuel;
XX industrial chemical; biodegradation; chloroaromatic;
XX environmental pollutant; Act1.
XX
XX Oryza sativa.
XX
XX WO200234926-A2.
XX
XX 02-MAY-2002.
XX
XX 18-OCT-2001; 2001WO-US032538.
XX
XX 20-OCT-2000; 2000US-0242408P.
XX
XX (UNMS ) UNIV MICHIGAN STATE.
XX
XX Sticklen MB, Dale BE, Magpool S;
XX
XX WPI; 2002-489947/52.
XX
XX Producing transgenic plants which after harvest degrade lignin and
XX cellulose to fermentable sugars, by mating transgenic plant comprising
XX DNA encoding cellulase with transgenic plant comprising DNA encoding
XX ligninase.
XX
XX Example 1; Page 124; 126pp; English.
XX
XX The invention discloses the production of a transgenic plant which
XX degrades lignocellulose when the plant is ground. It comprises the
XX production of the transgenic plant including cellulase and ligninase by
XX mating a transgenic plant, containing a DNA encoding a cellulase, and a
XX transgenic plant, containing a DNA encoding a ligninase, where both genes
XX are operably linked to a nucleotide sequence encoding a signal peptide
XX which targets the fusion protein to an organelle of the plant,
XX particularly chloroplasts. The method is useful for producing a
XX transgenic plant (e.g. maize) which degrades lignocellulose when the
XX plant is ground to produce a plant material. This material is useful for
XX converting lignocellulose, in a plant material, to fermentable sugars
XX which are then fermented to ethanol. The transgenic plants also provide a
XX plentiful and inexpensive source of fungal or bacterial cellulases and
XX ligninases which can be used in the production of ethanol. They can also
XX be used for pre-treating silage to increase the energy value of
XX lignocellulosic feeds for cows and other ruminant animals, pre-treating
XX lignocellulosic biomass for fermentative conversion to fuels and
XX industrial chemicals, and biodegradation of chloroaromatic environmental
XX pollutants. The sequence presented is the rice Act1 gene and promoter
XX
XX Sequence 623 BP; 98 A; 184 C; 164 G; 177 T; 0 U; 0 Other;
SQ
Query Match 27.2%; Score 426.2; DB 6; Length 623;
Best Local Similarity 87.3%; Pred. No. 3.4e-91;
Matches 504; Conservative 0; Mismatches 63; Indels 10; Gaps 3;
QY 991 ACACCTCCCAATTCACGCTGCGACCACTGCGGCTCTCCGCGCAAGCAACCAAGGAA 1050
|||||
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OY 1281 AATGGGCTCTCGATGTAGATCT--GATCGCGCGTTGTTGGGGAGATGATGGGCGTT 1338
    |||||
DB 5311 AATGGGCTCTCGATGTAGATCTGCGATCCGCGTTGTTGGGGAGATGATGGGCGTT 5370
    |||||
OY 1339 TAAATTTT-CGCCATGCTAAACAAGATCAGAGAAAGGGAAGGCACTATGCTTTATA 1397
    |||||
DB 5371 TAAATTTTCCGATGCTAAACAAGATCAGAGAAAGGGAAGGCACTATGCTTTATA 5430
    |||||
OY 1398 TTTTATATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1457
    |||||
DB 5431 TTTTATATATTTCTGCTGCT--TCGTCAGGCTTAGATGCTAGATCTTTCTTTCTCT 5488
    |||||
OY 1458 TTTTGGGAGTAGATTTGAATCCCTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1517
    |||||
DB 5489 TTTTGGGAGTAGATTTGAATCCCTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 5548
    |||||
OY 1518 TTGTGACAAATGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1565
    |||||
DB 5549 TTGTGACAAATGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5596
    |||||

RESULT 11
AAF80286
ID   AAF80286 standard; DNA; 9143 BP.
XX
XX   AAF80286;
XX
XX   29-JUN-2001 (first entry)
XX
XX   Nucleotide sequence of plasmid pMR1193.
XX
XX   Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;
KM   P382 protein; antibiotic resistance gene; nptIII; transgenic plant; ss.
XX
XX   Synthetic.
XX
XX   OS
XX   FH
XX   Key rep_origin
XX   Location/Qualifiers
XX   1..654
XX   /tag= a
XX   /note= "ori RK2"
XX   655..1263
XX   /tag= b
XX   /note= "ori COLE1"
XX   1264..2603
XX   /tag= c
XX   /note= "NPT III gene coding for neomycin
XX   phosphotransferase and kanamycin resistance"
XX   2604..4098
XX   /tag= d
XX   /note= "TrfA locus from RK2 coding for two proteins P285
XX   and P382 enabling an increase in the replication rate"
XX   4106..4271
XX   /tag= e
XX   /note= "T-DNA left border"
XX   4272..4559
XX   /tag= f
XX   /note= "NPT III gene coding for neomycin
XX   phosphotransferase and kanamycin resistance"
XX   4560..5556
XX   /tag= g
XX   /note= "NPT III gene coding for neomycin
XX   phosphotransferase and kanamycin resistance"
XX   5557..5770
XX   /tag= h
XX   /note= "nopaline synthetase promoter"
XX   5829..6254
XX   /tag= i
XX   /note= "high molecular weight glutenin promoter from
XX   wheat"
XX   6301..6833
XX   /tag= j
XX   /note= "rice actin intron"
XX   6834..8643
XX   /tag= k
XX   CDS
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FT /note= "GUS gene coding for beta glucuronidase"
FT 8644..8959
FT /tag= 1
FT /note= "nopaline synthetase terminator"
FT 8959..9136
FT /tag= m
FT /note= "T-DNA right border"
XX
XX FR2798139-A1.
XX
XX 09-MAR-2001.
XX
XX 03-SEP-1999; 99FR-00011112.
XX
XX 03-SEP-1999; 99FR-00011112.
XX
XX (MER1-) MERISTEM THERAPEUTICS SA.
XX
XX Gruber V, Comeau D;
XX
XX MPI; 2001-259847/27.
XX
XX New vector free from non-essential elements, useful for transforming
XX cells for protein production and for preparing transgenic plants.
XX
XX Claim 20; Page 124-127; 180pp; French.
XX
XX The specification describes a synthetic vector containing only those
XX elements essential for its functionality and transgenesis of a cell
XX (especially a plant cell). The vector consists of at most one origin of
XX replication (ori), at most one sequence encoding a selection agent and a
XX trfA locus encoding a protein that increases the level of plasmid
XX replication. The vector particularly contains an RK2 ori, especially oriV
XX from pRK2 of Escherichia coli with a broad host range, an antibiotic
XX resistance gene (especially nptIII conferring resistance to kanamycin in
XX bacteria) and a trfA locus from pRK2 encoding the proteins P285 and P382.
XX The vectors are used to prepare transgenic plants and transformed host
XX cells for production of a heterologous proteins, e.g. insulin,
XX interferon, lipase, blood proteins and anti-inflammatory agents. The
XX present sequence represents a plasmid of the invention
XX
XX Sequence 9143 BP; 2284 A; 2299 C; 2479 G; 2081 T; 0 U; 0 Other;
XX
XX Query Match 25.0%; Score 392; DB 4; Length 9143;
XX Best Local Similarity 93.0%; Pred No. 1.3e-82;
XX Matches 491; Conservative 0; Mismatches 20; Indels 17; Gaps 7;
OY 1053 GGCGCGCACCGCGGTGAGCTCTCCGCCCTCCCGCGCGC-----CGCGGTACC 1107
    |||||
DB 6278 GGCGCGCACCGCGGTGAGCTCTCCGCCCTCCCGCGCGCGCGCGGTAAAC 6337
    |||||
OY 1108 ACCCGCGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1166
    |||||
DB 6338 ACCCGCGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 6397
    |||||
OY 1167 GCCTGTGATTTGGGTGGGCGAGA----GCGGCTTCGTCGCGCAGATCGGTGCGGGA 1222
    |||||
DB 6398 GCCTGTGATTTGGGTGGGCGAGAAGCGGCTTCGTCGCGCAGATCGGTGCGGGA 6457
    |||||
OY 1223 GGCGCGGATCTCGCGGCTGCGCTCCG--GCGGTAGTCGACCGCGATCTCGCGGG 1280
    |||||
DB 6458 GGCGCGGATCTCGCGGCTGCGGCTCCGCGCGCGGTGATCCGCGCGGATCTCGCGGG 6517
    |||||
OY 1281 AATGGGCTCTCGATGTAGATCT--GATCGCGCGTTGTTGGGGAGATGATGGGCGTT 1338
    |||||
DB 6518 AATGGGCTCTCGATGTAGATCTGCGATCCGCGTTGTTGGGGAGATGATGGGCGTT 6577
    |||||
OY 1339 TAAATTTT-CGCCATGCTAAACAAGATCAGAGAAAGGGAAGGCACTATGCTTTATA 1397
    |||||
DB 6578 TAAATTTTCCGATGCTAAACAAGATCAGAGAAAGGGAAGGCACTATGCTTTATA 6637
    |||||
OY 1398 TTTTATATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1457
    |||||
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Db 6638 TTTTATATATTTCTGCTGCT--TCGTCAGGCTTAGATGTCATGATCTTTCTTCTCT 6695  
QY 1458 TTTTGGGGTAGAATTGGAATCCCTCAGCATGTTCATCCGTAAGTCTTTTCTTTCATGAT 1517  
Db 6696 TTTTGGGGTAGAATTGGAATCCCTCAGCATGTTCATCCGTAAGTCTTTTCTTTCATGAT 6755  
QY 1518 TTGTGAACAATGACGCTCGGCGAGCTTTTGTGTGGTAGAACCATG 1565  
Db 6756 TTGTGAACAATGACGCTCGGCGAGCTTTTGTGTGGTAGAACCATG 6803

RESULT 12  
AAF80295  
ID AAF80295 standard; DNA, 10003 BP.  
AC AAF80295;  
XX  
XX 29-JUN-2001 (first entry)  
XX  
XX Nucleotide sequence of plasmid pMR11210.  
XX  
XX Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;  
KM P382 protein; antibiotic resistance gene; nptIII; transgenic plant; ss.  
XX  
XX Synthetic.  
XX  
XX Key  
FH rep\_origin  
FT 1..654  
FT /tag= a  
FT /note= "ori RK2"  
FT 655..1263  
FT /tag= b  
FT /note= "ori COLE1"  
FT 1264..2603  
FT /tag= c  
FT /note= "NPT III gene coding for neomycin  
phosphotransferase and kanamycin resistance"  
FT 2604..4098  
FT /tag= d  
FT /note= "TrfA locus from RK2 coding for two proteins P285  
and P382 enabling an increase in the replication rate"  
FT 4106..4271  
FT /tag= e  
FT /note= "T-DNA left border"  
FT 4272..4559  
FT /tag= f  
FT /note= "nopaline synthetase terminator"  
FT 4594..5169  
FT /tag= g  
FT /note= "Bar gene coding for phosphinotricin  
acetyltransferase and glufosinate resistance"  
FT 5170..5704  
FT /tag= h  
FT /note= "rice actin intron"  
FT 5705..6638  
FT /tag= i  
FT /note= "rice actin promoter"  
FT 6672..7107  
FT /tag= j  
FT /note= "wheat high molecular weight glutenin promoter"  
FT 7169..7687  
FT /tag= k  
FT /note= "rice actin intron"  
FT 7688..9496  
FT /tag= l  
FT /note= "GUS gene coding for beta glucuronidase"  
FT 9497..9823  
FT /tag= m  
FT /note= "nopaline synthetase terminator"  
FT 9823..9996  
FT /tag= n  
FT /note= "T-DNA right border"

PN FR2798139-A1.  
XX  
XX PD 09-MAR-2001.  
XX PD 03-SEP-1999; 99FR-00011112.  
XX PF 03-SEP-1999; 99FR-00011112.  
XX PR 03-SEP-1999; 99FR-00011112.  
XX (MER1-) MERISTEM THERAPEUTICS SA.  
XX  
XX PI Gruber V; Comeau D;  
XX  
XX DR WPI; 2001-259847/27.  
XX  
XX PT New vector free from non-essential elements, useful for transforming  
XX cells for protein production and for preparing transgenic plants.  
XX  
XX PS Claim 20; Page 163-166; 180pp; French.  
XX  
XX CC The specification describes a synthetic vector containing only those  
XX elements essential for its functionality and transgenesis of a cell  
XX (especially a plant cell). The vector consists of at most one origin of  
XX replication (ori), at most one sequence encoding a selection agent and a  
XX trfA locus encoding a protein that increases the level of plasmid  
XX replication. The vector particularly contains an RK2 ori, especially oriV  
XX from pRK2 of *Escherichia coli* with a broad host range, an antibiotic  
XX resistance gene (especially nptIII conferring resistance to Kanamycin in  
XX bacterial) and a trfA locus from pRK2 encoding the proteins P285 and P382.  
XX The vectors are used to prepare transgenic plants and transformed host  
XX cells for production of a heterologous proteins, e.g. insulin,  
XX interferon, lipase, blood proteins and anti-inflammatory agents. The  
XX present sequence represents a plasmid of the invention  
XX  
SQ Sequence 10003 BP; 2476 A; 2470 C; 2729 G; 2328 T; 0 U; 0 Other;  
Query Match 25.0%; Score 392; DB 4; Length 10003;  
Best Local Similarity 93.0%; Pred. No. 1,4e-82;  
Matches 491; Conservative 0; Mismatches 20; Indels 17; Gaps 7;  
QY 1053 GGCAGCGACCGCGAGTGAAGTCTCCCTCCCTCCGCGC-----CGCGGTAAAC 1107  
Db 7131 GGCAGCGACCGCGAGTGAAGTCTCCCTCCCTCCGCGCGCGCGCGCGGTAAAC 7190  
QY 1108 ACCCGGCCCT 1166  
Db 7191 ACCCGGCCCT 7250  
QY 1167 GCCTTGATGTTGGGTGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1222  
Db 7251 GCCTTGATGTTGGGTGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 7310  
QY 1223 GGGGCGGAGTCTCGCGGCTGCGCTCCG--GGCGTGAATCGGCGCGATCTCGCGGAG 1280  
Db 7311 GGGGCGGAGTCTCGCGGCTGCGCTCCGCGCGGCGTGAATCGGCGCGATCTCGCGGAG 7370  
QY 1281 AATGGGCTCTCGATGATGATCT--GATCCGCGTGTGTGGGAGATGATGAGGCGGT 1338  
Db 7371 AATGGGCTCTCGATGATGATCTCGCGCGCGTGTGTGGGAGATGATGAGGCGGT 7430  
QY 1339 TAAATTTT--CGCATCTTAAACAAGTACAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1397  
Db 7431 TAAATTTTCCGCATCTTAAACAAGTACAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7490  
QY 1398 TTTTATATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1457  
Db 7491 TTTTATATATTTCTGCTGCT--TGTGAGGCTTGAATGATGATGATGATGATGATGATGATGAT 7548  
QY 1458 TTTTGGGGTAGAATTGGAATCCCTCAGCATGTTCATCCGTAAGTCTTTTCTTTCATGAT 1517  
Db 7549 TTTTGGGGTAGAATTGGAATCCCTCAGCATGTTCATCCGTAAGTCTTTTCTTTCATGAT 7608  
QY 1518 TTGTGAACAATGACGCTCGGCGAGCTTTTGTGTGGTAGAACCATG 1565

DB	7609	TTGTGACAAATGCAGCCTTCGTGGAGCTTTTGTGTAGTAGACCAAG	7656
		RESULT 13	
		ABT07357	
		ABT07357 standard; DNA; 470 BP.	
XX	AC	ABT07357;	
XX	XX	07-NOV-2002 (first entry)	
XX	XX	Reporter construct fragment rice actin intron SEQ ID NO: 109.	
XX	KW	Plant; gene expression control; insect; hormone receptor; fertility;	
XX	KW	ecdysone receptor; ds.	
XX	OS	Oryza sativa.	
XX	PN	WO200261102-A2.	
XX	PD	08-AUG-2002.	
XX	PP	24-OCT-2001; 2001WO-US051417.	
XX	PR	24-OCT-2000; 2000US-0242969P.	
XX	XX	(SYGN ) SYNGENTA PARTICIPATIONS AG.	
PI	PA	Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;	
XX	DR	WPI; 2002-619259/66.	
XX	XX	New receptor cassette encoding a chimeric receptor polypeptide, useful in	
PT	PT	regulating expression of target polypeptides in plants in the presence of	
PT	PT	appropriate ligands that may be used in controlling plant fertility.	
XX	PS	Example 10; Page 263; 319pp; English.	
CC	CC	The present invention relates to a receptor cassette encoding a chimeric	
CC	CC	receptor polypeptide comprising at least one DNA binding domain, a hinge	
CC	CC	domain of an ecdysone receptor (ECR) of an insect, a ligand binding	
CC	CC	domain of an insect ECR, where the ligand binding domain is heterologous	
CC	CC	with respect to the hinge domain and an activation domain. The chimeric	
CC	CC	insect hormone receptors and receptor cassettes are useful in regulating	
CC	CC	expression of target polypeptides in plants in the presence of	
CC	CC	appropriate ligands that may be used in controlling plant fertility. The	
CC	CC	method is useful for decreasing or increasing plant gene expression. The	
CC	CC	present sequence is a polynucleotide described in the exemplification of	
CC	CC	the invention	
SQ		Sequence 470 BP; 75 A; 103 C; 141 G; 151 T; 0 U; 0 Other;	
		Query Match 24.9%; Score 390.4; DB 6; Length 470;	
		Best Local Similarity 93.9%; Pred. No. 1e-82;	
		Matches 443; Conservative 0; Mismatches 16; Indels 13; Gaps 3;	
QY	1099	CGGTAACACACCCGCCCTCTCCCTCTTCTTCTCGGTTTTTTTTT-CGTCGCGCT	1157
DB	1	CGGTAAACACCCGCCCTCTCTCTTCTTCTTCTCGGTTTTTTTTTTCGCTCGGCT	60
QY	1158	CGATCTTGGCCTTGTAATTGGGTGGCGAGA---CGGCTTCGTGCGCCAGATCGG	1213
DB	61	CGATCTTGGCCTTGTAATTGGGTGGCGAGAAGCGGCTTCGTGCGCGCCAGATCGG	120
QY	1214	TGCGGGGAGGGCGGGAATCTGCGGGCTGGCGCTCTCGGCGGTGAATCGGCCGATCTT	1273
DB	121	TGCGGGGAGGGCGGGAATCTGCGGGCTGGCGG-----GGGCTTCGTGCGCGGTGAATCTT	172
QY	1274	CGCGGGGAATGGGGCTCTCGAATGTAATCGATCGCGCGTGTGGGGGAGATGATGGG	1333
DB	173	CGCGGGGAATGGGGCTCTCGAATGTAATCGATCGCGCGTGTGTGGGGGAGATGATGGG	232
QY	1334	GCATTAAATTTCCCATGTCTAAACAAGATCAGGAAGAGGGAAGAGGCACTATGGTT	1393

Db	233	GCCTTTAAATTTTGGCCATGCTAAACAGATCAGAAAGAGGAGAAAAGGCACATRTGTT	292
Qy	1394	TAAATTTTAAATATTTCTGCTGCTCGTCAAGCTTAAATGTCATAGATCTTTCTTTC	1453
Db	293	TAAATTTTAAATATTTCTGCTGCTCGTCAAGCTTAAATGTCATAGATCTTTCTTTC	352
Qy	1454	TTCTTTTGTGGAGAAATTGAAATCCCTGACATTTGTCATCGTAGTTTTCCTTTC	1513
Db	353	TTCTTTTGTGGAGAAATTGAAATCCCTGACATTTGTCATCGTAGTTTTCCTTTC	412
Qy	1514	TGAATTTGACAAATGCAGCTCGTGGAGACTTTTGTAGTGAACATG	1565
Db	413	TGAATTTGACAAATGCAGCTCGTGGAGACTTTTGTAGTGAACATG	464

RESULT 14
ID ADF49181 standard; DNA; 470 BP.
ADFA9181;
AC ADF49181;
DT 12-FEB-2004 (first entry)
DE Rice actin intron.
XX
KM receptor cassette; chimeric receptor polypeptide; DNA binding domain;
KW hinge domain; eclypsone receptor; Ecr; ligand binding domain;
KM activation domain; transgenic seed; transgenic plant; plant line;
KW herbicide; pesticide; rice; actin; intron; ds.
XX
OS Oryza sp.
OS
PN US2003154509-A1.
PN
PD 14-AUG-2003.
PD
PF 24-OCT-2001; 2001US-00087167.
PF
XX 24-OCT-2001; 2001US-00087167.
PR
XX
PA (PASC/) PASCAL E J.
PA (VALE/) VALENTINE S A.
PA (BROW/) BROWN J A.
PA (COCK/) COCKRELL A S.
PA (JOHN/) JOHNSON B D.
XX
PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
PI
DR WPI; 2003-897756/82.
XX
PT New receptor cassette encoding a chimeric receptor polypeptide, useful
PT for regulating the expression of target polypeptides in plants in the
PT presence of appropriate chemical ligands.
PT
XX
PS Example 10; SEQ ID NO 109; 186pp; English.
PS
XX The invention describes a receptor cassette encoding a chimeric receptor
XX polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
XX (D) domain of an eclypsone receptor (Ecr) of an insect, a ligand binding
XX (E) domain that is heterologous with respect to the D domain, and an
XX activation domain. The receptor cassette and method are useful in
XX regulating the expression of target polypeptides in plants in the
XX presence of appropriate chemical ligands. The transgenic seeds and plants
XX can be used for the breeding of improved plant lines that, for e.g.
XX increase the effectiveness of conventional methods such as herbicide or
XX pesticide treatment. This sequence represents a rice actin intron used in
XX the construction of a monocot-expressible target expression cassette
XX comprising the firefly luciferase reporter gene and having response
XX elements for the GAL4 DNA binding domain.
XX
XX Sequence 470 BP; 75 A; 103 C; 141 G; 151 T; 0 U; 0 Other;
XX



Db 8064 TCGTCGCGAGCTTTTGTAGTAGACC 8091

Search completed: September 12, 2005, 00:41:11  
Job time : 671.718 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2005, 23:36:11 ; Search time 4105.12 Seconds  
(without alignments)  
14511.284 Million cell updates/sec

Title: US-10-758-799-3

Perfect score: 1565  
Sequence: 1 GAATTCCTGAGAGTCGACG.....TTTTTGTAGTAGACCAAG 1565

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	222	14.2	776	9	CG005206 ZUAE95TH
2	221.2	14.1	293	8	CC001894 PUBC30TD
3	218.8	14.0	853	8	BZ791049 PUBG01TB
4	218.8	14.0	864	8	BZ808218 PUBG02TB
5	218.4	14.0	838	9	CG018790 ZUAE66TH
6	218	13.9	1008	9	CL998388 ZUAEH001
7	217.2	13.9	1026	9	CL998109 ZUAEH001
8	217.2	13.9	795	6	CD437903 EL01N0506
9	217.2	13.9	861	6	CD437903 EL01N0506
10	216.4	13.8	927	9	CL988337 ZUAEH000
11	216.2	13.8	807	9	CG152598 PUBH31TD
12	215.6	13.8	728	9	CG015128 ZUAEH000
13	215.6	13.8	874	9	CG196646 PUBDR84TB
14	214.4	13.7	646	9	CG082637 PUBLB06TD
15	214	13.7	890	8	BZ674680 PUBEO2TD
16	213.2	13.6	929	9	CG711569 CGICB93TH
17	213.2	13.6	1025	9	CL998355 ZUAEH001
18	213	13.6	782	9	CG347502 OCTDT19TV
19	213	13.6	927	9	CG172605 PUBF32TB
20	212.2	13.6	786	8	BZ978385 PUBIX48TD
21	212.2	13.6	982	9	CG152241 PUBDM51TD
22	211.8	13.5	944	8	CG338516 OGBG42TV
23	211	13.5	668	8	CC423224 PUBPZ66TB
24	210.8	13.5	737	9	CG738302 ZUAEH003

25	210.8	13.5	918	9	CG084733 PUKDU01TD
26	209.6	13.4	647	9	CG707522 119002G0
27	209.2	13.4	886	9	CG002179 ZUAEH000
28	208.6	13.3	837	8	CC338512 OGBG42TH
29	208.4	13.3	780	8	BZ988125 PUBSD60TB
30	208.2	13.3	704	8	BZ796630 PUBG90TD
31	207.8	13.3	1040	9	CL988912 ZUAEH000
32	207.8	13.3	1085	9	CL990459 ZUAEH000
33	206.8	13.2	761	8	BZ755899 PUBCG4TB
34	206.4	13.2	776	8	CC356868 PUBH62TD
35	206.4	13.2	919	8	CC426863 PUBK30TB
36	206.2	13.2	830	8	BZ796628 PUBGK90TB
37	206.2	13.2	973	9	CL994908 ZUAEH000
38	205.2	13.1	948	8	CC383150 PUBH052TD
39	205.6	13.1	640	8	BZ804749 PUBG547TD
40	205.2	13.1	714	9	CG013617 ZUAEH000
41	205.2	13.1	777	9	CG356927 OGBA02TV
42	205.2	13.1	778	9	CG356921 OGBA02TV
43	205.2	13.1	786	9	CG175670 PUBH35TD
44	205.2	13.1	801	9	CG015229 ZUAEH000
45	205.2	13.1	821	8	CC010502 PUBDA07TD

## ALIGNMENTS

RESULT 1  
CG005206/c  
LOCUS ZUAE95TH ZM 3.0 4.0 KB Zee may genomic clone ZUAE95TH, 776 bp  
DEFINITION genomic survey sequence.  
ACCESSION CG005206  
VERSION CG005206.1 GI:33876322  
KEYWORDS GSS.  
SOURCE Zee may  
ORGANISM Zee may

## REFERENCE

Whitehead, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robb, D. and Lakey, N.  
1 (bases 1 to 776)  
Clade: Panicoideae; Andropogoneae; Zee.

## TITLE

Unpublished (2002)  
Other GSSs: ZUAE95TV  
Contact: Cathy Whitehead  
TI:GR  
712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitehead@ti-gr.org  
Seq primer: TR  
Class: sheared ends.

## FEATURES

Location/Qualifiers  
1..776  
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/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="ZUAE95TH1022"  
/clone\_1b="ZM 3.0 4.0 KB"  
/note="Vector: pBCSK-; Site\_1: HincII; 3-4 kb 'unfiltered' genomic DNA library"

## ORIGIN

Query Match 14.2% Score 222; DB 9; Length 776;  
Best Local Similarity 79.3%; Pred. No. 4.2e-41;  
Matches 303; Conservative 0; Mismatches 70; Indels 9; Gaps 3;

214 GGGCTTACATCATCATCATCATCATCTTCGCGTGTCTCTTAAAGATTCATCTCT 273  
Db 635 GTCTCTATATCATCTCTATATCTCTTACAGTCTTCTTAAAGATTCATCTCT 576

[illegible]

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RESULT 2
CC001894
LOCUS
DEFINITION CC001894 293 bp DNA linear GSS 31-MAR-2003
PUBBC30TDD ZM_0.6_1.0_KB Zea mays genomic clone ZM8BTa196B11,
genomic survey sequence.
ACCESSION CC001894
VERSION CC001894.1 GI:29380454
KEYWORDS GSS.
SOURCE
ORGANISM Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 293)
WhiteIaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
Rennick,A., Frazer,C.M., Yuan,Y., San Miguel,P., Ma,D. and
Benetzen,J.
Maize Genomics Consortium
Unpublished (2003)
Contact: Cathy WhiteIaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whiteIaw@tigr.org
Seq primer: TP
Class: sheared ends.
FEATURES
Source location/Qualifiers
1..293
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZM8BTa196B11"
/clone_lib="ZM_0.6_1.0_KB"
/note="vector: pCR4-ToPO; Site_1: EcoRI, 0.6-1.0 kb high
cot selected genomic DNA library"
ORIGIN

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Query Match	14.1%	Score 221.2	DB 81	Length 293
Best Local Similarity	89.7%	Pred. No. 5.7e-41		
Matches 278	Conservative 0	Mismatches 13	Indels 19	Gaps 3

  

OY	610	CGGTATTTTGGCGATGGCGCCTCTCATATTTTCACTCCACGC-CCCCACATTTTACGTT	667
Db	1	CGGTATTTTGGCGATGGCGCCTCTCATATTTTCAACGAGGCGCCCTCTCTTTTACGTT	60

QY	668	TTCAACCGAAGGCCGACGTGCCTTAACCAACAATAATGGTAAGGTGGCGGGTTTCAAAA	727
Db	61	TTCAACCGAAGGCCCA-----GCCAACCAACAATAATGGTAAGGTGGCGGGTTTCAAAA	116
QY	728	GAAGTCCGAAACCATCTTGACACCCACCGCATAGTAGGCCCTCGGATCTCCTCGATTAAAT	787
Db	117	GAAAGCCGAAACCATCTTGACACCCACCGCATAGTAGGCCCTCGGATCTCCTCGATTAAAT	176
QY	788	CCTGAGCCATAATGAGAGCCGAGAACCAACCATACAGCGGATTCGGTCCCTAGCGTTCCACCTCA	847
Db	177	CCTGAGCCATAATGAGAGCCGAGAACCAACCATATACGGGATTCGTCCCTAGCGTTCCACCTCA	236
QY	848	TCGGAGCGCGTCATCTCCATCCAAACCACTATTCGGTTACCTTGACCCATCTCTCGAAAAAA	907
Db	237	TCGGAGCGCGTCATCTCCATCCAAACAATA-----CCATCTCTCGAAAAAA	283
QY	908	TTCTCGGCTC 917	
Db	284	TTCTCGGCTC 293	

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RESULT 3
BZ791049
LOCUS      BZ791049          853 bp    DNA         linear   GSS 17-MAR-2003
DEFINITION PUFGD01TB ZM_0.6_l.0_KB Zea mays genomic clone ZMMBT311B02,
            genomic survey sequence.
ACCESSION  BZ791049
VERSION    BZ791049.1  GI:28987056
KEYWORDS   GSS.
SOURCE     Zea mays
            Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 853)
            WhiteLaw C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
            Renick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
            Bennetzen, J.
            Maize Genomics Consortium
            Unpublished (2003)
OTHER GSSs: PUFGD01TD
CONTACT: Cathy WhiteLaw
TIGR       9712 Medical Center Drive, Rockville, MD 20850, USA
           Tel.: 301-838-5843
           Fax: 301-838-0208
           Email: whiteLaw@cigr.org
Seq primer: TR
Class: sheared ends.

FEATURES             location/Qualifiers
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	Query Match	14.0%;	Score 218.8;	DB 8;	Length 853;
	Best Local Similarity	79.7%;	Pred. No. 2.4e-40;		
	Matches 298;	Conservative 0;	Mismatches 67;	Indels 9;	Gaps 3.
QY	214	GGCCTTACATCCATCTATATATCCATCCTTTCCGGTGTCTCTAAAGAATTCATCCT	273		
DB	33	GTCCCTATATTCATCTCTATATCCGTTCTTTACAGATATCTAAAGAATTTATCCT	92		
QY	214	CTGAATCTATATCCCTCCCATATAGTCTCTAATCAGAGCTGTATAA--GCATACCT	331		
DB	93	CTATATCTCTTTCTCTCCCAACAGCTTCTTAAATCAGGCTCTTATATCTCAAAATATCT	152		

Oy	332	ATATTAGAGACAT-----TTTATATTTTGGACATACATATTGTCACTACTCAAT	385
Db	153	ATATTAGACATTTTATTATTTTATTTTGTACATACGATTTGTTATCTCCAAAT	212
Oy	386	GCATTATACATA-TTACTTTTACTAAACCGATTATTTAAAGATTTCAAACGATGANGA	444
Db	213	GTATTGTGCAATATTTAGTTTGTCTAAACCGGTATTTTAAAGATTTCAAATGGATMAAGG	272
Oy	445	ACTGTTTGAATTAATTTCTATATATATAGAGAAATCAGTAGCGTCTCTAAATTTAGATGATT	504
Db	273	ACCGTTTAGAGAAACTCTATATATATAGAGAAATCAGACCGTCTCTAAATTTAGAGAAC	332
Oy	505	ATTTAGAGACGCGTGTAGAAAAAGTAAAAAATTCCTTGATTATTTATATTTTAAAGGTAGA	564
Db	333	GTTTTAGAGACGCGTCTGAGAGCATAGAGATCAATTGATTCCTTATATTTTAAAGGTACA	392
Oy	565	GTAGCCTTATGCT	578
Db	393	GAACCTTTAGGCT	406

RESULT 4	BZ808218	864 bp	DNA	linear	GSS 17-MAR-2003
LOCUS	BZ808218				
DEFINITION	BZ808218	PUGGC02TB_ZM_0.6.1.0_KB	zea mays	genomic clone ZMMBT5311B03,	
ACCESSION	BZ808218				
VERSION	BZ808218.1	GI:29020571			
KEYWORDS	GSS,				
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
AUTHORS	Whitelaw C.A., Quackenbush, J., Van Aken, S., Uterback, T., Renwick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennerzen, J.				
TITLE	Maize Genomics Consortium				
JOURNAL	Unpublished (2003)				
COMMENT	Other_GSSs: PUGGC02TD				

9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: [Whitelaw@tlgr.org](mailto:Whitelaw@tlgr.org)  
Seq primer: TR  
Class: sheared ends.

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Query Match	14.0%;	Score 218.8;	DB 8;	Length 864;
Best Local Similarity	79.7%;	Pred. NO. 2.4e-40;		
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QY	274	CTGAATCTTATTCCTCTGCATATACGTTCTCTAAATCAGGTCTCTATTA--GCAATACCT	331
Db	98	CTATATCTCTTCTCTCTCCAAACAGGTTCTCTAAATCAGGTCTCTATATCTCAATATCT	157

Oy	332	ATTATGAGACAT-----TTTTATTTTTTGATCATGATTTTGGCATACCTCAAT	385
Db	158	ATATGAGACATTTTTTATTTTTTATTTTTTTGGACATACGATTTTGTATATCTCAAT	217
Oy	386	GCAATTATACATA-TTTAGTTTACTAACCAGTATTTAAAGTATCAAAAGATGAGA	444
Db	218	GTATTTGACATTTTATAGTTTGTGTAACCGGTATTTTAAAGTATCAAAAGATGAGAAGG	277
Oy	445	ACATGTTAGTAAATCTATATATATAGAGATCCAGTAGCCTCTCTAAATTTAGATGAT	504
Db	278	ACCGTTTAGAGAACTCTATATATATAGAGATCCAGACGCTCTCTAAATTTAGAGACC	337
Oy	505	ATTTAGAGACGCTGTTAGAAAACGTAAAAAATCTTGATTTATTTATTTAGGGTAGA	564
Db	338	GTATTAGAGACGCTGCTGAGAGAGCATAGAGATCATTTGATCTCTATATTTAGGGTACA	397
Oy	565	GTAGCCTTTATGCT	578
Db	398	GAAACCTTTAGGCT	411

RESULT 5	CG018790	838 bp	DNA	linear	GSS 19-AUG-2003			
LOCUS	ZUAE666TH ZM.3.0.4.0 KB	zea mays	genomic clone	ZMMBPa043L11,				
DEFINITION	genomic survey sequence.							
ACCESSION	CG018790							
VERSION	CG018790.1	GI:33890955						
KEYWORDS	GSS.							
SOURCE	Zea mays							
ORGANISM	Zea mays							
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.							
REFERENCE	1 (bases 1 to 838)							
AUTHORS	Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Renick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nurnberg, A., Robbins, D. and Lakey, N.							
TITLE	Consortium for Maize Genomics							
JOURNAL	Unpublished (2002)							
COMMENT	Other_GSSs: ZUAE666TV							

9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: [white1aw@tigr.org](mailto:white1aw@tigr.org)  
Seq primer: TR  
Class: sheared ends.

FEATURES	source	Location/Qualifiers
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Query Match	14.0%;	Score 218.4;	DB 9;	Length 838;
Best Local Similarity	80.4%;	Pred. No. 3e-40;		
Matches 307; Conservative	0;	Mismatches 66;	Indels 9;	Gaps 4

QY 21 GGCCTAACATCATCATATATATATCATATCTTCGAGTCTCTTAAAGATTCATCCT 273  
Db 6 GTCTCTAATTCATCTCTTATCTGATCGATCTTCAAGTCTCTCTCTTAAAGATTCATCCT 65  
QY 274 CTGATCTTATTCCTCTCGAATAAGTTCCTAAATGAGT-CTCTTAAAGC-AATTCCT 3311  
Db 66 CTATATCTATATCTCTTCAACAAGTCTCTTAATTCAGATCTTATACTCAAAATATCT 1258

QY	332	ATTATTAGAGACATTTTTLTA-----TTTTTGGACATGATATTGTGCATCTCAAT	385		
Db	126	ATTATTAGAGACATTTTTLTAATTGTTGTTTTTATACATACGATTTGTCTACTCCAAAT	185		
QY	386	GCATTATACATA-TTTAGTTTTTACTAAACCGATTATTTTAAAGATATTCACACGATGAAGA	444		
Db	186	GTATTATGACATATTTTGGTTTTTGTCTAAACCGGTATTATTTAAAGTATTCACAAATGGATAGAG	245		
QY	445	ACTGTTTATGATTAATTTCTATATATATAGAAATTCAGTACCGTTCTCTAAATTTAATTAATGATT	504		
Db	246	ACCGTTTATGACAAATCTATATGATATGAAATTCACACGATTCCTTAAATTTTAAAGGAGACC	305		
QY	505	ATTATGAGAGACGCTTCTAGAAACGTAAAAAATTCCTTGATTTATTTATTTAGGGTGA	564		
Db	306	GTTTATGAGAGACGCTCTGAGAGCATGAGAGCATTGGTCTCTATATATTTAGGGTACA	365		
QY	565	GTAGCCTTTATGCTTTATATAGAT	586		
Db	366	GACCCCTTATGAGGTCTTGGCT	387		
RESULT 6	CLJ98388	1008 bp	DNA	linear	GSS 23-SEP-2004
LOCUS	ZMNBHf001ln01.f	ZMNBHf Zea mays	genomic clone	ZMNBHf001ln01 5',	
DEFINITION	ZMNBHf001ln01.f	ZMNBHf Zea mays	genomic clone	ZMNBHf001ln01 5',	
ACCESSION	CLJ98388				
VERSION	CLJ98388.1	GI:52570043			
KEYWORDS	GSS.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCES	Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
AUTHORS	Ma,J., SamiGuel,P., Liu,R., Haller,K., Soderlund,C. and Bennezen,J.				
TITLE	ZMNBH sequences				
JOURNAL	Unpublished (2004)				
COMMENT	Contact: Jeff Bennezen Bennezen Lab The University of Georgia Department of Genetics, C426a Life Sciences Building, Athens, GA 30602, USA Tel: 706-542-3698 Fax: 706-583-0972 Email: maize@uga.edu Plate: 0011 row: n column: 01 Class: BAC ends.				
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Query Match	13.9%;	Score 218;	DB 9;	Length 1008;	
Best Local Similarity	78.7%;	Pred. No. 3.8e-40;			
Matches	285;	Conservative 0;	Mismatches 75;	Indels 2;	Gaps 2
QY	214	GAGCTTACATCATCATATATATCATATCTTTCCGGTCTCTTAAAGATTCATCT	273		
Db	264	GTCCCTATATTCATTATCTATATATCCGTCCTTACATCATCTTAAAGATTTATCT	323		
QY	274	CTGATCTTATCTCTCCATTAACAGTTCTCTAATTCAGTCTCTATTAAGC-AAATACCTA	332		

Dc	324	CATATATCTTGCCCTCCTCAACAACGATTCCTAATATACGCTCCCTATATGCCAAATATCA	383
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Dd	384	TATTAGAGATATTTTATTTATTTTGTATATACGATTTATCATCTCCAAATGTAATGT	443
Qy	393	ACATA-TTTAGTTTACTAAACCGATTATTTAAAGTATTTAAACGGATGAAGAAGCTGTT	451
Dd	444	ACATATTTTAGTTTGTCTAAACCGATTATTTAAAGTATTTCAAATGGATAGATGGCGCTT	503
Qy	452	AGATAATCTATATATAGAGATCCAGTAGCGTTCTCTAAATTTAGATGATTATTAGA	511
Dd	504	AAAAAACCTCTATATATAGAGATCCAGTAGAGTTCTCTAAATTTAGAGGACCGTTTAA	563
Qy	512	GAGCGCTGTAGAAAACGTAAAAATTCCTTGATTATTTATTTAGGGTAGAGTAGCCT	571
Dd	564	GAGCACCTGTAAAGCGCTAGAGGACCGATTAAAACTCTATATTATTTAGAGTACGAAGAGCT	623
Qy	572	TT	573
Dd	624	TT	625

RESULT 7	CL998109	1026 bp	DNA	linear	GSS 23-SEP-2004
LOCUS	ZMMBHf0011h03.f	ZMMBHf0011h03 5',			
DEFINITION	genomic survey sequence.				
ACCESSION	CL998109				
VERSION	CL998109.1	GI:52569489			
KEYWORDS	GSS.				
SOURCE	Zea mays				
ORGANISM	Zea mays				

REFERENCE  
AUTHORS  
TITLE  
ZMMB sequences

TITLE ZMMBH sequences  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Jeff Bennettzen  
 Bennettzen lab  
 The University of Georgia  
 Department of Genetics, C426a Life Sciences Building, Athens, GA  
 30602, USA  
 Tel: 706-542-3698  
 Fax: 706-583-0972  
 Email: maize@uga.edu  
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 Class: BAC ends.

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Best Local Similarity	78.7% ; Pred. No. 3,88-40 ;	
Matches 285; Conservative	0; Mismatches 75; Indels 2; Gaps 2;	
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OY	274	CGAATCTTATTCCTCTCCAAATAAGGTTCTCAAAATCAGGTCCTATAAGC--ATAACCTA	332
Db	324	CTATTAATCTTCCCTCCCAACAAAGGTTCTCAAAATCAGGTCCTATAAGCAAAATCTCA	383
OY	333	TATTAGAGACATTTTATATTTTGGTACATACATATTTGGTCMACTCTCAATGCAATTAT	392
Db	384	TATTAGAGATATTTTATATTTTGGTATATATAGCAATTATCACTCTCAATGTAATTCGT	443
OY	393	ACATA--TTTAGTTTTACTAAACCGATTATTTAAAGTATCAAAACGATGAAGAATGTGTT	451
Db	444	ACATATTTTAGTTTGGCTAAACCAAGTATTTAAAGATTAACAATGGAATGATGGCGGCTT	503
OY	452	AGATTAATTTCTATATATATAGAGATCCAGTAGCGTTCTCAAAATTTAGATGATTAATTGACA	511
Db	504	AAAAAAACCTCTATATATATAGAGATCCAGCAGAGTTCTCAAAATTTTAGAGAACCGTTTGA	563
OY	512	GGAGCGCTGTGAAAAACGTAAAAAATCTTTGATATTTATATATTTAGGTAAGTAGACCT	571
Db	564	GGACACTGCTAAAGAGCGTAGAGACCGATTAAAACTCTATATTTTAGAGATACAGAAGGCT	623
OY	572	TT 573	
Db	624	TT 625	

RESULT 8	CD437903	795 bp	mRNA	linear	EST 03-JUN-2003
LOCUS	CD437903				
DEFINITION	EL0105050610.b Endoperm_5	Zea mays	CDNA,	mRNA	sequence.
ACCESSION	CD437903				
VERSION	CD437903.1	GI:31353546			
KEYWORDS	EST.				
SOURCE	Zea mays				
ORGANISM	Zea mays				

REFERENCE

Bukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 795)

REFERENCE	1 (bases 1 to 795)
AUTHORS	Lai, J., Day, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F.,
TITLE	larkin, B. Beckett, P. and Messing, J.
JOURNAL	Characterization of the maize endosperm transcriptome and its
COMMENT	comparison to the rice genome
	Genome Res. 14 (10), 1932-1937 (2004)
	Contact: Lai, Jinsheng

Waksman Institute, Rutgers University  
195 Fellingnugnysen Rd., Piscataway, NJ 08854, USA  
Tel.: 732-445-3801  
Fax: 732-445-5735  
Email: j1a@waksman.rutgers.edu  
Seq primer: T3

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Location/Qualifiers
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## ORIGIN

Query Match	Score	DB	Length
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Best Local Similarity 78.5%; Pred. No. 5.7e-40;  
Matches 300; Conservative 0; Mismatches 73; Indels 9; Gaps 3;

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Db 324 GTCCCTATATTCATCCTATATCCGCTTTTACAGTCTCCTCTAAAGATTCTATCCT 383

274 CTGAATCTATTCCTCTCCAATAACGTTCTCTAATCAGGTCCTATAA--GCAATACCT 331

Db 384 CTATCTCTCCCTCCTCCGACCAAGCGTCTCTAAATCAAGTCTCTATCTCAAAATATCT 443

Qy 382 ATATTAGAGACT-----TTTATATTTTGTACATACATATTTGTCAATCTCAAAAT 385

Db 444 ATATTAGAAACATTTTATATTTTATTTTATTTTGTACATACATATTTGTCAATCTCAAAAT 503

Qy 386 GCATTATATACATA-TTATAGTTTACTAAACGATTTATTTAAAGTATTCAAACGATGAAGA 444

Db 504 GTATTGTATATTTTATAGTTTGTCAAAACCAAGTTATTTTAAAGATTTCAATATGATAGAG 563

Qy 445 ACTGTTTAGATTAATTCTATATATATAGAGAAATCCAGTAGGTTCTCTAAATTTTAGATGATT 504

Db 564 ACCGTTTAGAAGAACTCTATATATATTAAGAAATCCAGAGCGAATCTTAAATTTTAGAGACT 623

Qy 505 ATTTAGAGAGACGCTGTAGAAAAACGTAAAAAATCTTTGATTAATTTATATTTTAGGGTAGA 564

Db 624 GTTTTAGAGAGACGCTGCTGGAGGCGTAGAGTACCAATTTGATCCTATATTTTAGGGTAGA 683

Qy 565 GTAGCCTTATAGCTTTATAGAT 586

Db 684 GAACCTTTAGGGTTCCTTGCT 705

RESULT 9			
CD437683			
LOCUS	CD437683	861 bp	mRNA
DEFINITION	E010IN503H03. b EndospERM_5 Zea mays cDNA, linear EST 03-JUN-2003, mRNA sequence.		

DEFINITION	EL01N0503H03.b EndospERM__5 Zea mays cDNA, mRNA sequence.
ACCESSION	CD437683
VERSION	CD437683.1 GI:3153326
KEYWORDS	EST.
SOURCE	Zea mays
ORGANISM	Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta, Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE  
AUTHORS  
1 (bases 1 to 861)  
Lai, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F.,  
Larkins, B., Bercraft, P. and Messing, J.

TITLE	JOURNAL	COMMENT
Characterization of the maize endosperm comparison to the rice genome	Genome Res. 14 (10), 1932-1937 (2004)	Contact: Lai, Jinsheng Institute of Molecular Biology

Maksman Institute, Rutgers University  
130 Frelinghuysen Rd., Piscataway, NJ 08854, USA  
Tel.: 732-445-3801  
Fax: 732-445-5735  
Email: jla@maksman.rutgers.edu  
Seq primer: T3

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XhoI"

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Query Match 13.9%; Score 217.2; DB 6; Length 861;

Matches 300; Conservative 0; Mismatches 73; Indels 9; Gaps 3;

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274 CTGATCTTATTCCTCTCCAATAACGTTCTCTAATCAGGTCCTATAA--GCAATACCT 331

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QY 332 ATATTAGACAT-----TTTTTATTTTGTACATACATATTGTCTCAATCTCAAAAT 385  
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 QY 505 ATTTAGAGACGCTGTTAGAAAACGTAAAAAATTTCTTGATTTATATTTTAGGCTAGA 564  
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RESULT 10  
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 LOCUS ZMBHe005f06.r ZMBHe Zea mays genomic clone ZMBHe005f06 3',  
 DEFINITION genomic survey sequence.  
 ACCESSION CL988337  
 VERSION CL988337.1 GI:52556415  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays

REFERENCE  
 AUTHORS Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 1 (bases 1 to 988)  
 Ma,J., SanMiguel,P., Liu,R., Haller,K., Soderlund,C. and  
 Bennetzen,J.  
 ZMMB sequences  
 Unpublished (2004)

TITLE  
 JOURNAL  
 COMMENT

Contact: Jeff Bennetzen  
 Bennetzen Lab  
 The University of Georgia  
 Department of Genetics, C426a Life Sciences Building, Athens, GA  
 30602, USA  
 Tel: 706-542-3698  
 Fax: 706-583-0972  
 Email: maize@uga.edu  
 Plate: 0005 Row: f column: 06  
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 Location/Qualifiers

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# ORIGIN

Query Match 13.8%; Score 216.4; DB 9; Length 988;  
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 Db 264 GTCTCTAGTCTATATATCTATATCTGCTCTTACATCTACTCTAAGATTTTATCT 323  
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 QY 274 CTGAATCTTATTCCTCTCAATAACGTTCTCTAATCAGTCTCTATAGC-ATACTTA 332  
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 QY 572 TT 573  
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RESULT 11  
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 ACCESSION CG152598  
 VERSION CG152598.1 GI:34043393  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays

REFERENCE  
 AUTHORS Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 1 (bases 1 to 807)  
 Whiteclaw,C.A., Quackenbush,J., Van Aken,S., Uteerpack,T.,  
 Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
 Bennetzen,J.  
 Maize Genomics Consortium  
 Unpublished (2003)

TITLE  
 JOURNAL  
 COMMENT

Contact: Cathy Whiteclaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whiteclaw@tigr.org  
 Seq primer: TF  
 Class: sheared ends.  
 Location/Qualifiers

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RESULT 12

LOCUS	728 bp	DNA	GSS 23-SEP-2004
DEFINITION	ZMMLC0007E02.r ZMMLC Zea mays genomic clone ZMMLC0007E02 3',		
ACCESSION	ZMMLC0007E02		
VERSION	ZMMLC0007E02.1		
KEYWORDS	GSS.		

## ORGANISM

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD  
clade; Panicoideae; Andropogoneae; Zea.

## AUTHORS

TITLE ZMML sequences  
JOURNAL Unpublished (2004)  
COMMENT Contact: Rod A. Wing

Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: <http://genome.arizona.edu>  
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Class: BAC ends.

**SOUT**

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### RESULT 13

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DEFINITION PUJ8984TB\_ZM\_0\_6\_1\_0\_KB Zea mays genomic clone ZMNBTA0644N24,  
genomic survey sequence.

**VERSION**

**KEYWORDS** GSS.

**SOURCE** Zee maven

## ORGANISM

Eukaryota; Viridiplantae; streptophyta; emoryophyta; iracnophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD clade; Panicoideae; Andropogoneae; Zea.

## AUTHORS

**TITLE** Maize Genomics Consortium  
**FORMING** Benneken, J.  
Keshnick, A., Friesel, C.W., Iwata, T., San Miguel, P., Ma, B. and  
Reynolds, L.P.

## COMMENT

Contact: Cathy Whitelaw  
iRGR Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5863  
Fax: 301-838-0208  
Email: whitelaw@iRGR.org  
Seq primer: TR  
Class: sheared ends.

**sour**

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## ORIGIN

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Best Local Similarity	78.3%	Pred. No. 1.4e-39		
Matches 299	0	Mismatches 74	Indels 9	Gaps 3

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 00:10:11 ; Search time 220.914 Seconds  
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Title: US-10-758-799-3

Perfect score: 1565  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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3	454	29.0	454	4	US-09-037-531-2	Sequence 2, Appl1
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6	428.8	27.4	2199	1	US-08-144-6028-5	Sequence 5, Appl1
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8	426.2	27.2	623	3	US-09-078-862-5	Sequence 5, Appl1
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## ALIGNMENTS

## RESULT 1

US-09-037-531-3  
Sequence 3, Application US/09037531

Patent No. 6750378  
GENERAL INFORMATION:

APPLICANT: Frey, Richard

ATTORNEY/AGENT INFORMATION: Maize H3C4 Promoter Combined With The

TITLE OF INVENTION: First Intron Of Rice Actin, Chimeric Gene Comprising It

TITLE OF INVENTION: And Transformed Plant

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Connolly, Bove, Lodge, & Hutz

STREET: 1220 Market Street

CITY: Wilmington

STATE: DE

COUNTRY: USA

ZIP: 19899

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

Application Number: US/09/037, 531

FILING DATE: 10-MAR-1998

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: McMorrow Jr., Robert G.

REGISTRATION NUMBER: 30962

REFERENCE/DOCKET NUMBER: 5500\*24

TELECOMMUNICATION INFORMATION:

TELEPHONE: (302)658-9141

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1565 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-037-531-3

Query Match

Best Local Similarity 100.0%; Score 1565; DB 4; Length 1565;

Matches 1565; Conservative 0; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2  
US-09-037-531-1  
Sequence 1, Application US/09037531  
Patent No. 6750378  
GENERAL INFORMATION:  
Applicant: DeRose, Richard  
Title of Invention: Maize H3C4 Promoter Combined With The  
Title of Invention: First Intron Of Rice Actin, Chimeric Gene Comprising It  
Number of Sequences: 5  
Correspondence Address:  
Address: Connolly, Bove, Lodge, & Hutz  
Street: 1220 Market Street  
City: Wilmington  
State: DE  
Country: USA  
ZIP: 19899  
COMPUTER READABLE FORM:  
Medium Type: Floppy disk  
Computer: IBM PC compatible  
Operating System: PC-DOS/MS-DOS  
Software: Patent Release #1.0, Version #1.25  
Current Application Data:  
Application Number: US/09/037,531  
Filing Date: 10-MAR-1998  
Classification: 800  
Attorney/Agent Information:  
Name: McMorow Jr., Robert G.  
Registration Number: 30962  
Reference/Docket Number: 5500\*24  
Telecommunication Information:  
Telephone: (302)658-9141  
Information for SEQ ID NO: 1:  
Sequence Characteristics:  
Length: 1021 base pairs  
Type: nucleic acid  
Strandedness: single  
Topology: linear  
Molecule Type: DNA (genomic)  
US-09-037-531-1



Query Match 65.2%; Score 1021; DB 4; Length 1021;  
Best Local Similarity 100.0%; Pred. No. 1.2e-272; Indels 0; Gaps 0;  
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QY 267 CCAATCCTGTAATCTTATCTCTCAATACGTTCTCAATACAGGTTCTCAATACAA 326
DB 241 CCAATCCTGTAATCTTATCTCTCAATACGTTCTCAATACAGGTTCTCAATACAA 300
QY 327 TACCTATATTAGAGACATTTTATTTTGTATACATATTTTGTATCTCTCAATG 386
DB 301 TACCTATATTAGAGACATTTTATTTTGTATACATATTTTGTATCTCTCAATG 360
QY 387 CATTAATACATATTAGTTTACTAAACGATTAATTAAGATTAATTAAGATTAAGAT 446
DB 361 CATTAATACATATTAGTTTACTAAACGATTAATTAAGATTAATTAAGATTAAGAT 420
QY 447 TGTATGATTAATTTCTATATATAGAGATCCAGTAGCGTTCTCAATTTAGATGAT 506
DB 421 TGTATGATTAATTTCTATATATAGAGATCCAGTAGCGTTCTCAATTTAGATGAT 480
QY 507 TTAGAGAGCGCTGTAGAAAAGTAAATTTCTTGAATTTATTTAGGGTAGAGT 566
DB 481 TTAGAGAGCGCTGTAGAAAAGTAAATTTCTTGAATTTATTTAGGGTAGAGT 540
QY 567 AGCCTTATGCTTATATGATCTTTGGGAGCCGCTTATACCGGTTATTTTCGCGAT 626
DB 541 AGCCTTATGCTTATATGATCTTTGGGAGCCGCTTATACCGGTTATTTTCGCGAT 600
QY 627 GCGCTCTCAATTTCACTCCAGCGCCCAATTTTCAAGTTTCAAGAAAGCCGCGCC 686
DB 601 GCGCTCTCAATTTCACTCCAGCGCCCAATTTTCAAGTTTCAAGAAAGCCGCGCC 660
QY 687 TGCTTAACCAAAATTTGTAGCGGTGCGCGGTTTCAAAAGAAAGTGGAAACCATGTC 746
DB 661 TGCTTAACCAAAATTTGTAGCGGTGCGCGGTTTCAAAAGAAAGTGGAAACCATGTC 720
QY 747 ACCGACCGATGTAAGGCGCTCGGATCTCTCCATTAAGTCTTACGCAATAGAGGCCA 806
DB 721 ACCGACCGATGTAAGGCGCTCGGATCTCTCCATTAAGTCTTACGCAATAGAGGCCA 780
QY 807 GAAACACCATCAAGCGGATCGTCCCTCAAGCTTCACTCATAGGCGCGCTTCACTCCA 866
DB 781 GAAACACCATCAAGCGGATCGTCCCTCAAGCTTCACTCATAGGCGCGCTTCACTCCA 840
QY 867 TCGAACACCTATTCCTGTAATCTTGCATCTTCGGAATAATTCCTGCGCTCGCG 926
DB 841 TCGAACACCTATTCCTGTAATCTTGCATCTTCGGAATAATTCCTGCGCTCGCG 900
QY 927 ACCGACGTAATTAATCCATCCATCAAGAGCAATGATGATGCGCAATCCCCCGAATA 986
DB 901 ACCGACGTAATTAATCCATCCATCAAGAGCAATGATGATGCGCAATCCCCCGAATA 960
QY 987 ATCAACACCTCCCAATTCAGAGCTGCGCAACATCGCGCTCTCGCGCGCAAGCAACAA 1046
DB 961 ATCAACACCTCCCAATTCAGAGCTGCGCAACATCGCGCTCTCGCGCGCAAGCAACAA 1020
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QY 1047 G 1047  
DB 1021 G 1021

## RESULT 3

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US-09-037-531-2
; Sequence 2, Application US/09037531
; Patent No. 6750378
; GENERAL INFORMATION:
; APPLICANT: Derose, Richard
; TITLE OF INVENTION: Maize H3C4 Promoter Combined With The
; TITLE OF INVENTION: First Intron Of Rice Actin, Chimeric Gene Comprising It
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/037,531
; FILING DATE: 10-MAR-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorrow Jr., Robert G.
; REGISTRATION NUMBER: 30962
; REFERENCE/DOCKET NUMBER: 5500*24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302)658-9141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-037-531-2
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Query Match 29.0%; Score 454; DB 4; Length 454;

Best Local Similarity 100.0%; Pred. No. 1.2e-115; Indels 0; Gaps 0;

Matches 454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1102 GTAACACCCCGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1161
DB 1 GTAACACCCCGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
QY 1162 CTTTGGCTTTGTAATTTGGGTTGGGAGAGCGGCTTCTGCGCCAGATCGTGCGGG 1221
DB 61 CTTTGGCTTTGTAATTTGGGTTGGGAGAGCGGCTTCTGCGCCAGATCGTGCGGG 120
QY 1222 AGGGGGGGGATCTCGGGGCTGCGGCTCTCGGGGCTGAGTCCGCGCGGATCTCGGG 1281
DB 121 AGGGGGGGGATCTCGGGGCTGCGGCTCTCGGGGCTGAGTCCGCGCGGATCTCGGG 180
QY 1282 ATGGGCTCTCGGATGATGATCGGCTCGGCTGTTGGGGAGATGATGAGGGCGTTTAA 1341
DB 181 ATGGGCTCTCGGATGATGATCGGCTCGGCTGTTGGGGAGATGATGAGGGCGTTTAA 240
QY 1342 AATTTGCGATGCTAAACAAGATGAGAAAGAGGGGAAAAGGCACTATGTTATTTTT 1401
DB 241 AATTTGCGATGCTAAACAAGATGAGAAAGAGGGGAAAAGGCACTATGTTATTTTT 300
QY 1402 TATATATTTCTGTCGTGCTGCGGCTTAAAGTGTAGATCTTTCTTTCTTTT 1461
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; NAME/KEY: misc feature
; LOCATION: (4016)..(4021)
; OTHER INFORMATION: Label = Kpn1, "Kpn1 recognition site"
US-09-970-921-5

Query Match          24.2%; Score 378.4; DB 4; Length 4032;
Best Local Similarity 87.1%; Pred. No. 4e-94;
Matches 498; Conservative 0; Mismatches 61; Indels 13; Gaps 7;

QY 1004 CCAAGCTGACCAACCACTCCGCGCTCCCGGCAAGACCAAGAAATGGCCGCAACG 1063
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1064 CCGTGGAGCTCTCCCGCCCTCCCGCCGCGCGCGGAAACACCCGCTCTCTCT 1123
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2895 AGCTCTCCCGCCCTCCCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2953
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1124 CTTTCTTTCTCCGTTTTTTTTT-CGTCTCGATCTCGATCTTTGGCTTTGGATGG 1182
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2954 CTTTCTTTCTCCGTTTTTTTTTCCGCTCGATCTCGATCTTTGGCTTTGGATGG 3013
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1183 TGGGCGGAGA---GCGGCTTCGTCCCAATCGGTCCGCGGAGGCGGAGATCTCCG 1238
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3014 TGGGCGGAGGCGGCTTCGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3073
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1239 GCTGGCGTCTCCG--GCGTGAATCGGCGCGGATCCCTCGGCGGAAATGGGCTCTCG 1296
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3074 GCTGGGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3133
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1297 GTAGATCT--GATCCGCGCTTGTGGGAGATGATGAGGCGTTTAAATTT-CGCGAT 1353
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3134 GTAGATCTGGATCCGCGCTTGTGGGAGATGATGAGGCGTTTAAATTT-CGCGAT 3193
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1354 CTAAACAATCGAAGAGAGGAGAAAGGCACTATGTTTATTTTATTTATTTCTG 1413
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3194 CTAAACAATCGAAGAGAGGAGAAAGGCACTATGTTTATTTTATTTATTTCTG 3253
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1414 CTGCTGCTCGAGGCTTATGATGCTGATCTTTCTTTCTTTTGTGGTAGAAT 1473
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3254 CTGCT--TGTCTAGGCTTATGATGCTGATCTTTCTTTCTTTTGTGGTAGAAT 3311
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1474 TGAATCCCTCAGCATTTGTCATCGTATGTTTCTTTCTTATGATTTGTGAACAATG 1533
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QY 1534 CTGCTGCGAGGCTTTTGTAGTAGAATG 1565
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QY 3372 CTGCTGCGAGGCTTTTGTAGTAGAATG 3403
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RESULT 11
US-09-377-466B-19
; Sequence 19, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 3039
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; NAME/KEY: Promoter
; LOCATION: (14)..(235)
; OTHER INFORMATION: P-CMV.AS4
; NAME/KEY: 5'UTR
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; LOCATION: (240)..(304)
; OTHER INFORMATION: L-Ta.hcbl
; NAME/KEY: Intron
; LOCATION: (318)..(805)
; OTHER INFORMATION: I-Os.Act1
; NAME/KEY: CDS
; LOCATION: (811)..(2769)
; OTHER INFORMATION: Cry3Bd1 variant 11231mw1
; NAME/KEY: terminator
; LOCATION: (2787)..(3020)
; OTHER INFORMATION: T-Ta.hcpl7
US-09-377-466B-19

Query Match          24.0%; Score 375.8; DB 4; Length 3039;
Best Local Similarity 93.2%; Pred. No. 1.8e-93;
Matches 450; Conservative 0; Mismatches 22; Indels 11; Gaps 5;

QY 1087 CCTCCGCGCGCGGTAACACACCCGCCCTCTCTCTTTCTTCTCGTTTTTTTT 1146
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 319 CCTCCGCGCGCGCGGTAACACACCCGCCCTCTCTCTTTCTTCTCGTTTTTTTT 378
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1147 CGTCTCGCTCGATCTTTGGCTTGTAGTTTGGGTGGGCGAGA---GCGCTTCGT 1202
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 379 CGTCTCGCTCGATCTTTGGCTTGTAGTTTGGGTGGGCGAGA---GCGCTTCGT 438
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1203 GCCAGATCGTGGCGGAGGCGGAGCTCGCGCTGCGCTCCG--GCGTGAAT 1260
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 439 GCCAGATCGTGGCGGAGGCGGAGCTCGCGCTGCGCTCCGCGCGCGCTCGAT 498
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1261 CGGCGCGATCTCGCGGGAATGGGCGCTCTCGATGATGATCT--GATCCGCTTGT 1318
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 499 CGGCGCGATCTCGCGGGAATGGGCGCTCTCGATGATGATCTCGATCTCGCTTGT 558
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1319 GGGGAGATGATGGGCGTTTAAATTT--CGCATGCTTAAACAATGAGAGGGGA 1377
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 559 GGGGAGATGATGGGCGTTTAAATTTCCGCGCTTAAACAATGAGAGGGGA 618
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1378 AAAGGCACTATGTTTATTTTATTTATTTCTGCTGCTGCTGAGCTTATGAT 1437
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QY 619 AAAGGCACTATGTTTATTTTATTTATTTCTGCTGCTGCTGAGCTTATGAT 676
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QY 1438 GCTAGATCTTTCTTTCTTTTGTGGTAGAATTTGATCTCTGAGATTTGATCG 1497
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 677 GCTAGATCTTTCTTTCTTTTGTGGTAGAATTTGATCTCTGAGATTTGATCG 736
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1498 GTAGTTTCTTTTATGATTTGTGAACAATGCAACCTCGTGGAGCTTTTGTAGGT 1557
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 737 GTAGTTTCTTTTATGATTTGTGAACAATGCAACCTCGTGGAGCTTTTGTAGGT 796
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QY 1558 AGA 1560
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 797 AGA 799
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 12
US-09-377-466B-21
; Sequence 21, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 3039
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; OTHER INFORMATION: cassette
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; SEQ ID NO 38
; LENGTH: 3044
; TYPE: DNA

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 :  
 : CURRENT APPLICATION NUMBER: US/09/377,466B  
 :  
 : CURRENT FILING DATE: 1999-08-19  
 :  
 : NUMBER OF SEQ ID NOS: 43  
 :









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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 02:27:12 ; Search time 1992.88 Seconds  
(without alignments)  
5157.238 Million cell updates/sec

Title: US-10-758-799-3

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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7351250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications NA.\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1565	100.0	9	US-09-037-531-3	Sequence 3, Appl
2	1565	100.0	19	US-10-758-799-3	Sequence 1, Appl
3	1021	65.2	1021	US-09-037-531-1	Sequence 1, Appl
4	1021	65.2	1021	US-10-758-799-1	Sequence 1, Appl
5	454	29.0	454	US-09-037-531-2	Sequence 2, Appl
6	454	29.0	454	US-10-758-799-2	Sequence 2, Appl
7	426.2	27.2	623	US-09-961-9008-19	Sequence 19, Appl

	8	402.8	25.7	2480	21	US-10-678-588A-1	Sequence 1, Appl
c	9	402.8	25.7	5365	22	US-10-839-092-57	Sequence 57, Appl
	10	392.8	25.1	1384	22	US-10-839-092-35	Sequence 35, Appl
	11	392	25.0	7943	10	US-09-845-064-15	Sequence 15, Appl
	12	392	25.0	9143	10	US-09-845-064-12	Sequence 12, Appl
	13	392	25.0	10003	10	US-09-845-064-21	Sequence 21, Appl
	14	390.4	24.9	470	16	US-10-087-167-109	Sequence 109, App
	15	384.8	24.6	9359	21	US-10-344-977A-1	Sequence 1, Appl
	16	384.8	24.6	9359	22	US-10-344-975B-1	Sequence 1, Appl
	17	381.2	24.4	7794	24	US-11-057-062-2	Sequence 2, Appl
	18	381.2	24.4	8590	24	US-11-057-062-1	Sequence 1, Appl
	19	378.4	24.2	4032	9	US-09-970-921-5	Sequence 5, Appl
	20	376.8	24.1	1597	22	US-10-839-092-50	Sequence 50, Appl
	21	375.8	24.0	491	9	US-09-376-940-50	Sequence 50, Appl
	22	375.8	24.0	3034	20	US-10-841-796-34	Sequence 34, Appl
	23	375.8	24.0	3039	15	US-10-233-665-19	Sequence 19, Appl
	24	375.8	24.0	3039	15	US-10-233-665-21	Sequence 21, Appl
	25	375.8	24.0	3044	15	US-10-233-665-38	Sequence 38, Appl
	26	375.8	24.0	3450	15	US-10-233-665-17	Sequence 17, Appl
	27	375.8	24.0	3455	15	US-10-233-665-36	Sequence 36, Appl
	28	375.8	24.0	3469	15	US-10-233-665-23	Sequence 23, Appl
	29	375.8	24.0	6865	10	US-09-845-064-13	Sequence 13, Appl
c	30	375.8	24.0	10003	10	US-09-845-064-21	Sequence 21, Appl
	31	375.8	24.0	11546	20	US-10-841-796-33	Sequence 33, Appl
	32	358.8	22.9	12378	15	US-10-213-791-27	Sequence 27, Appl
	33	358.8	22.9	8296	24	US-11-057-062-1	Sequence 1, Appl
	34	352.8	22.5	4176	24	US-11-057-062-7	Sequence 7, Appl
	35	352.8	22.5	4176	24	US-10-213-791-29	Sequence 29, Appl
	36	310.2	19.8	2122	15	US-10-213-791-25	Sequence 25, Appl
	37	247.8	15.8	1259	10	US-09-991-209-43	Sequence 43, Appl
	38	247.8	15.8	4773	10	US-09-991-209-32	Sequence 32, Appl
	39	247.8	15.8	4950	10	US-09-991-209-34	Sequence 34, Appl
	40	247.8	15.8	4965	10	US-09-991-209-37	Sequence 37, Appl
	41	247.8	15.8	4974	10	US-09-991-209-35	Sequence 35, Appl
	42	247.8	15.8	5164	10	US-09-991-209-36	Sequence 36, Appl
	43	247.8	15.8	5277	10	US-09-991-209-25	Sequence 25, Appl
	44	247.8	15.8	5285	10	US-09-991-209-38	Sequence 38, Appl
	45	247.8	15.8	5327	10	US-09-991-209-27	Sequence 27, Appl

#### ALIGNMENTS

RESULT 1  
US-09-037-531-3  
Sequence 3, Appl  
Patent No. US2002010417A1  
GENERAL INFORMATION:  
APPLICANT: Defose, Richard  
TITLE OF INVENTION: Freysinet, Georges  
TITLE OF INVENTION: Matize H3C4 Promoter Combined With The  
TITLE OF INVENTION: First Inventor Of Rice Actin, Chimeric Gene Comprising It  
TITLE OF INVENTION: And Transformed Plant  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESS: Connolly, Bove, Lodge, & Hutz  
STREET: 1220 Market Street  
CITY: Wilmington  
STATE: DE  
COUNTRY: USA  
ZIP: 19899  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/037,531  
FILING DATE: 10-MAR-1998  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: McMorrow Jr., Robert G.  
REGISTRATION NUMBER: 30962

REFERENCE/DOCKET NUMBER: 5500\*24  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (302)658-9141  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1565 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-09-037-531-3

Query Match 100.0%; Score 1565; DB 9; Length 1565;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GAATTCCTGAGGTGACGAGATCCCTTATGTGACCATTTACTGTATGATATCAT 60
DB 1 GAATTCCTGAGGTGACGAGATCCCTTATGTGACCATTTACTGTATGATATCAT 60
QY 61 TTAATGAAAGAACTTTCTATTAATCTTTACTTAACAATATCTGGTTTAAAT 120
DB 61 TTAATGAAAGAACTTTCTATTAATCTTTACTTAACAATATCTGGTTTAAAT 120
QY 121 TCAGTCTCAACATTCATGCTCAAGTATAGTGAAGTCAAAATTTACTATTAT 180
DB 121 TCAGTCTCAACATTCATGCTCAAGTATAGTGAAGTCAAAATTTACTATTAT 180
QY 121 TCAGTCTCAACATTCATGCTCAAGTATAGTGAAGTCAAAATTTACTATTAT 180
DB 121 TCAGTCTCAACATTCATGCTCAAGTATAGTGAAGTCAAAATTTACTATTAT 180
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DB 241 TCCCTTCCGGTGTCTTAAAGATTCATCCCTGATCTTATCTCTCCAAATACGT 300
QY 301 TCTCTAATCAGGTCTCTAATAGCAATACCTATATTAGAGACATTTTTTATTTTGTAC 360
DB 301 TCTCTAATCAGGTCTCTAATAGCAATACCTATATTAGAGACATTTTTTATTTTGTAC 360
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QY 481 AGCGTCTCTAATTTAGATGATTTATTAGAGACGCTGTAGAAAAAGTAAATTCCT 540
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DB 541 TTGATTATTTATATTTAGGATAGTAGACCTTTATGCTTATATAGATCTTTGTGACCA 600
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DB 601 GCGTTATACCGGTATTTTGGCAATGGCGCTCTCATTTTCACTCCAGGCCCCCAATTT 660
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DB 601 GCGTTATACCGGTATTTTGGCAATGGCGCTCTCATTTTCACTCCAGGCCCCCAATTT 660
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QY 720 TCACGTTTTCACGGAAGCGCCAGCGCTGCTTAACCAACAATTTGTTACGCGGCTT 720
DB 720 TCACGTTTTCACGGAAGCGCCAGCGCTGCTTAACCAACAATTTGTTACGCGGCTT 720
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DB 721 TTCAAAAGAAATCGGAAACCATCTGACCCAGGACTAGTAGGCGCTCGGATCTTCCCT 780
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DB 781 ATTAAGTCTTAAGCAATAGAGGCCAGAACCAACCATCAAGCGGATGTCTTACGCTTC 840
QY 841 CACCTCATCGGCGCGCTCATCTCATCAACACCTATTCGTTACCTTCCATCTCTC 900

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DB 841 CACCTCATCGGCGCGCTCATCTCATCAACACCTATTCGTTACCTTCCATCTCTC 900
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DB 901 GAAAAAATTTCTCGGCTCGCGCTCTCCGACCTACTCAATATCCATCCATCAAGCGGAT 960
QY 961 CGCATCACTGCAGAAATCCCAAGAAATCAACACCTCCCAATTTCCACGCTGCACCAACT 1020
DB 961 CGCATCACTGCAGAAATCCCAAGAAATCAACACCTCCCAATTTCCACGCTGCACCAACT 1020
QY 1021 CGCGGTCTCTCGGCGCAAGCACCAAGAAATTTGCGCCACCGCGGTGAGTCTCTCCCC 1080
DB 1021 CGCGGTCTCTCGGCGCAAGCACCAAGAAATTTGCGCCACCGCGGTGAGTCTCTCCCC 1080
QY 1081 CCTCCCGCTCGCGCGCGCGGTAAACAACCGCGCGCTCTCTCTTTCTTTCTCCGTTT 1140
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QY 1141 TTTTTCGTCTCGATCTTGATCTTTGAGTGTGAGTGGGCGAGAGCGGCTTCG 1200
DB 1141 TTTTTCGTCTCGATCTTGATCTTTGAGTGTGAGTGGGCGAGAGCGGCTTCG 1200
QY 1201 TCGCCCAAGTCGTTGCGGGAAGGCGGATCTTCGCGCTGCGCTCTCCGCGCTGAGT 1260
DB 1201 TCGCCCAAGTCGTTGCGGGAAGGCGGATCTTCGCGCTGCGCTCTCCGCGCGTGA 1260
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DB 1261 CGGCGCGGATCTCGCGGGAAGTGGGGGCTCTCGAGATGATGATCGCGCGTGTGG 1320
QY 1321 GGGAGATGATGGGGGCTTTAAATTTCCCATGCTTAAACAAGATCAGAGAAGGAGAAA 1380
DB 1321 GGGAGATGATGGGGGCTTTAAATTTCCCATGCTTAAACAAGATCAGAGAAGGAGAAA 1380
QY 1381 GGGCACTATGTTTATATTTTATATATTTTCTGCTGCTGCTGCTGAGCTTATGATGCT 1440
DB 1381 GGGCACTATGTTTATATTTTATATATTTTCTGCTGCTGCTGCTGAGCTTATGATGCT 1440
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QY 1501 GTTTTCTTTTATATTTTGAACAATGCAAGCTCTGTCGGAAGCTTTTGTAGTAGA 1560
DB 1501 GTTTTCTTTTATATTTTGAACAATGCAAGCTCTGTCGGAAGCTTTTGTAGTAGA 1560
QY 1561 CCATG 1565
DB 1561 CCATG 1565

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RESULT 2  
 US-10-758-799-3  
 ; Sequence 3, Application US/10758799  
 ; Publication No. US2004019944A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dekose, Richard  
 ; Freysinet, Georges  
 ; TITLE OF INVENTION: Maize H3C4 Promoter Combined With The  
 ; First Intron Of Rice Actin, Chimeric Gene Comprising It  
 ; And Transformed Plant  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: Connolly, Bove, Lodge, & Hutz  
 ; STREET: 1220 Market Street  
 ; CITY: Wilmington  
 ; STATE: DE  
 ; COUNTRY: USA  
 ; ZIP: 19899  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible

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? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
?   APPLICATION NUMBER: US/10/758,799
?   FILING DATE: 16-Jan-2004
?   CLASSIFICATION: 800
? PRIOR APPLICATION DATA:
?   APPLICATION NUMBER: US/09/037,531
?   FILING DATE: 10-MAR-1998
? ATTORNEY/AGENT INFORMATION:
?   NAME: McMorow Jr., Robert G.
?   REGISTRATION NUMBER: 30962
?   REFERENCE/DOCKET NUMBER: 5500*24
? TELECOMMUNICATION INFORMATION:
?   TELEPHONE: (302)658-9141
? INFORMATION FOR SEQ ID NO: 3:
?   SEQUENCE CHARACTERISTICS:
?     LENGTH: 1565 base pairs
?     TYPE: nucleic acid
?     STRANDEDNESS: single
?     TOPOLOGY: linear
?     MOLECULE TYPE: DNA (genomic)
?     SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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US-10-758-799-3

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TITLE OF INVENTION: First Intron Of Rice Actin, Chimeric Gene Comprising It  
TITLE OF INVENTION: And Transformed Plant  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Connolly, Bove, Lodge, & Hutz  
STREET: 1220 Market Street  
CITY: Wilmington  
STATE: DE  
COUNTRY: USA  
ZIP: 19899  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/037,531  
FILING DATE: 10-MAR-1998  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: McMorrow Jr., Robert G.  
REGISTRATION NUMBER: 30962  
REFERENCE/DOCKET NUMBER: 5500\*24  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302)658-9141  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1021 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-037-531-1

Query Match 65.2%; Score 1021; DB 9; Length 1021;  
Best Local Similarity 100.0%; Pred. No. 9.3e-229;  
Matches 1021; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

27 CTTATGCGACCACTTATGCTGTAATGCAATATCATTTAATGAGAACTTTCTATT 86  
1 CTTATGCGACCACTTATGCTGTAATGCAATATCATTTAATGAGAACTTTCTATT 60  
87 ACTCTTTTACTAATCATATCTTGTGTTTAAATTCAGTCTCAACATTCATTCCTCAAG 146  
61 ACTCTTTTACTAATCATATCTTGTGTTTAAATTCAGTCTCAACATTCATTCCTCAAG 120  
147 TATAGTGGAGCTGTCGAAATTTACTATTATTTCTTCATATTTTCTTCTTATACA 206  
121 TATAGTGGAGCTGTCGAAATTTACTATTATTTCTTCATATTTTCTTCTTATACA 180  
207 CATTGTTGGGCTTACATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 266  
181 CATTGTTGGGCTTACATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 240  
267 CCATCCTCTGAATCTTATCTCTCCATATACGTTCTTAATCAGGCTCTTAATGCA 326  
241 CCATCCTCTGAATCTTATCTCTCCATATACGTTCTTAATCAGGCTCTTAATGCA 300  
327 TACCTATATTAGAGACATTTTATTTTGTATCATATTTTGTATCTCTCAATG 386  
301 TACCTATATTAGAGACATTTTATTTTGTATCATATTTTGTATCTCTCAATG 360  
387 CATTATACATATTAGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 446  
361 CATTATACATATTAGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 420  
447 TGTATGATTAATTTCTATATATAGAGATCCAGTAGCGTCTCTAATTTAGATGATAT 506  
421 TGTATGATTAATTTCTATATATAGAGATCCAGTAGCGTCTCTAATTTAGATGATAT 480  
507 TTAGAGAGCGCTGTAGAGAAACGTAAGAAATTTCTTGTATTTATTTATTTAGGATGAGT 566  
481 TTAGAGAGCGCTGTAGAGAAACGTAAGAAATTTCTTGTATTTATTTATTTAGGATGAGT 540

567 ACCCTTATGCTTATAGATCTTTGTGAGACCACTTATACCGTTATTTTCCGATT 626  
541 ACCCTTATGCTTATAGATCTTTGTGAGACCACTTATACCGTTATTTTCCGATT 600  
627 GCGCTCTGATTTTCACTTCAGCGCCCAATTTTCAAGTTTCAACGAGCGCCAGCC 686  
601 GCGCTCTGATTTTCACTTCAGCGCCCAATTTTCAAGTTTCAACGAGCGCCAGCC 660  
687 TGCCTTACCAAAATTTGGTATGATGGGCGGCTTTTCAAAAGATCGGAAACCATCTGC 746  
661 TGCCTTACCAAAATTTGGTATGATGGGCGGCTTTTCAAAAGATCGGAAACCATCTGC 720  
747 ACCCAACGACTGTATGAGCGCTCGATTCCTCTGATTAAGTCTTACCAATAGAGCCCA 806  
721 ACCCAACGACTGTATGAGCGCTCGATTCCTCTGATTAAGTCTTACCAATAGAGCCCA 780  
807 GAACCAACCATGAGCGGATGCTCTTACGTTTCACTCATGAGCGCGCTCATCTCCA 866  
781 GAACCAACCATGAGCGGATGCTCTTACGTTTCACTCATGAGCGCGCTCATCTCCA 840  
867 TCCACACCTATTCGTTACCTTGGCCATCCCTCGAAATAATTCGAGCTGCGGCTCGGC 926  
841 TCCACACCTATTCGTTACCTTGGCCATCCCTCGAAATAATTCGAGCTGCGGCTCGGC 900  
927 ACTTACTAATAATACCATTCATCCATGACGAGCATGCACTGACCAATCCCGAGAA 986  
901 ACTTACTAATAATACCATTCATCCATGACGAGCATGCACTGACCAATCCCGAGAA 960  
987 ATCAACACCTCCCAATTTCCAGCTGCGACCAACTGCGGCTCTCCGCGCAAGCAAA 1046  
961 ATCAACACCTCCCAATTTCCAGCTGCGACCAACTGCGGCTCTCCGCGCAAGCAAA 1020  
1047 G 1047  
1021 G 1021

RESULT 4  
US-10-758-799-1  
Sequence 1, Application US/10758799  
Publication No. US2004019944A1  
GENERAL INFORMATION:  
APPLICANT: Derose, Richard  
Freysinet, Georges  
TITLE OF INVENTION: Maize H3CA Promoter Combined With The  
First Intron Of Rice Actin, Chimeric Gene Comprising It  
And Transformed Plant  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Connolly, Bove, Lodge, & Hutz  
STREET: 1220 Market Street  
CITY: Wilmington  
STATE: DE  
COUNTRY: USA  
ZIP: 19899  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/758,799  
FILING DATE: 16-Jan-2004  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/037,531  
FILING DATE: 10-MAR-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: McMorrow Jr., Robert G.  
REGISTRATION NUMBER: 30962  
REFERENCE/DOCKET NUMBER: 5500\*24  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (302) 658-9141  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1021 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-758-799-1

Query Match 65.2%; Score 1021; DB 19; Length 1021;  
Best Local Similarity 100.0%; Pred. No. 9.3e-229; Index 0; Gaps 0;  
Matches 1021; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 27 CTTATGTGACCACTTACTGTAAATGCAATATCAATTTAATGAATAGCAAACTTTCTATT 86
DB 1 CTTATGTGACCACTTACTGTAAATGCAATATCAATTTAATGAATAGCAAACTTTCTATT 60
QY 87 ACTTCTTTACTAATATATCTGTTTAAATTCAGTCTCAACATTCATGCTCAG 146
DB 61 ACTTCTTTACTAATATATCTGTTTAAATTCAGTCTCAACATTCATGCTCAG 120
QY 147 TATAGTGTGACGTGCAAAATTTAATTTTCTGATATTTTCTGATATTTTCTGATATTA 206
DB 121 TATAGTGTGACGTGCAAAATTTAATTTTCTGATATTTTCTGATATTTTCTGATATTA 180
QY 207 CATTTTGGGCTTACATCCATCATCTATATCCATCTTCCGCTGCTCTAAAGATT 266
DB 181 CATTTTGGGCTTACATCCATCATCTATATCCATCTTCCGCTGCTCTAAAGATT 240
QY 267 CCATCTCTGATCTTATCTCTCCAAATACGTTCTTAAATCAGGCTCTTAAAGCA 326
DB 241 CCATCTCTGATCTTATCTCTCCAAATACGTTCTTAAATCAGGCTCTTAAAGCA 300
QY 327 TACCTATATAGAGACATTTTATTTTGTATCATATCATATTTGATCTCAAG 386
DB 301 TACCTATATAGAGACATTTTATTTTGTATCATATCATATTTGATCTCAAG 360
QY 387 CATTAATCATATTTAGTTTACTTAAACGATATTTTAAATTTTAAATTTTAAATTTTAAAT 446
DB 361 CATTAATCATATTTAGTTTACTTAAACGATATTTTAAATTTTAAATTTTAAATTTTAAAT 420
QY 447 TGTATGATTAATTTCTATATATAGAGATCCAGTAGCGTTCTTAAATTTAGATATAT 506
DB 421 TGTATGATTAATTTCTATATATAGAGATCCAGTAGCGTTCTTAAATTTAGATATAT 480
QY 507 TTAGAGAGCGCTGTAGAAAAGTAAATTTCTTTGATATTTTATTTAGGTAGAGT 566
DB 481 TTAGAGAGCGCTGTAGAAAAGTAAATTTCTTTGATATTTTATTTAGGTAGAGT 540
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DB 541 AGCCTTATATCTTATATGATCTTTGGGAGCCAGCTTATACCGGTTATTTTCGAGATT 600
QY 627 GCGCTCTCTATTTTCACTCCAGCGCCCAATTTTCACTTTTCAACGGAAGCGCCAGCC 686
DB 601 GCGCTCTCTATTTTCACTCCAGCGCCCAATTTTCACTTTTCAACGGAAGCGCCAGCC 660
QY 687 TGTCTAACCAAAATTTGTAGCGGTGCGGGTTTCAAAAGAGTGGAAACATCTTGC 746
DB 661 TGTCTAACCAAAATTTGTAGCGGTGCGGGTTTCAAAAGAGTGGAAACATCTTGC 720
QY 747 ACCCAACGATAGAGCGCTCGGATCTCTCGATTAATGCTTGAAGCAATAGAGGCCA 806
DB 721 ACCCAACGATAGAGCGCTCGGATCTCTCGATTAATGCTTGAAGCAATAGAGGCCA 780
QY 807 GAACCAACCATCAAGCGGATCTCTCGATTAATGCTTGAAGCAATAGAGGCCA 866
DB 781 GAACCAACCATCAAGCGGATCTCTCGATTAATGCTTGAAGCAATAGAGGCCA 840
QY 867 TCAAGACATATTCGTTACCTTGGCCATCTCCGAAAATTTCTGGGCTCGGCTCGC 926
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QY 927 ACTTACTAATAATACCATCCATCCATGACGAGCGATGCACTGCGCAATATCCCGAGAA 986
DB 901 ACTTACTAATAATACCATCCATCCATGACGAGCGATGCACTGCGCAATATCCCGAGAA 960
QY 987 ATCAACACTCCCAATTTCCAGCGTGCACCAACTGCGGCTCTCGGCGCAAGACCAAA 1046
DB 961 ATCAACACTCCCAATTTCCAGCGTGCACCAACTGCGGCTCTCGGCGCAAGACCAAA 1020
QY 1047 G 1047
DB 1021 G 1021
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RESULT 5  
US-09-037-531-2  
; Sequence 2, Application US/09037531  
; Patent No. US20020104117A1  
; GENERAL INFORMATION:  
; APPLICANT: Dekose, Richard  
; APPLICANT: Freysinet, Georges  
; TITLE OF INVENTION: Maize H3C4 Promoter Combined With The  
; TITLE OF INVENTION: First Intron Of Rice Actin, Chimeric Gene Comprising It  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Connolly, Bove, Lodge, & Hutz  
; STREET: 1220 Market Street  
; CITY: Wilmington  
; STATE: DE  
; COUNTRY: USA  
; ZIP: 19899  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/037,531  
; FILING DATE: 10-MAR-1998  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMorrow Jr., Robert G.  
; REGISTRATION NUMBER: 30962  
; REFERENCE/DOCKET NUMBER: 5500\*24  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (302) 658-9141  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 454 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-09-037-531-2

Query Match 29.0%; Score 454; DB 9; Length 454;  
Best Local Similarity 100.0%; Pred. No. 4.9e-96;  
Matches 454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GTAAACACCCCGCCCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 60
QY 1162 CTTTGGCTTTGGATTTGGGTTGGGAGAGGCGGCTTGTGCGCCAGATCGGTCGCGG 1221
DB 61 CTTTGGCTTTGGATTTGGGTTGGGAGAGGCGGCTTGTGCGCCAGATCGGTCGCGG 120
QY 1222 AGGGGCGGATCTCGGCGTGGGCTTCCGGCGTGAAGTCGAGCCGAGATCTTCCGCGGGA 1281
DB 121 AGGGGCGGATCTCGGCGTGGGCTTCCGGCGTGAAGTCGAGCCGAGATCTTCCGCGGGA 180
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/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (6834)..(8643)
/ OTHER INFORMATION: GUS gene coding for beta glucuronidase
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/ FEATURE:
/ NAME/KEY: terminator
/ LOCATION: (8644)..(8959)
/ OTHER INFORMATION: No. US20030175976AlaIaline synthetase terminator
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/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (8959)..(9136)
/ OTHER INFORMATION: T-DNA right border
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US-09-845-064-12
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Query Match      25.0%; Score 392; DB 10; Length 9143;
Best Local Similarity 93.0%; Pred. No. 7.8e-81;
Matches 491; Conservative 0; Mismatches 20; Indels 17; Gaps 7;
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QY 1053 GGGCGCACCGCGGTGAGCTCTCCCTCCCTCCCGCGC-----CGCCGTAACC 1107
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QY 1108 ACCCGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1166
DB 6338 ACCCGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 6397
QY 1167 GCCTTGTAAGTTGGGTGGGCGGAGA----GGGCTTCGTGCGCCAGATCGTGGCGGGA 1222
DB 6398 GCGTGTGTGTGGGTGGGCGGAGAGCGGCTTCGTGCGCGCCAGATCGTGGCGGGA 6457
QY 1223 GGGCGCGGATCTCGCGGCTGCGCTCTCCG--GGCGTAGTGGCGCGCGATCTCGCGGG 1280
DB 6458 GGGCGCGGATCTCGCGGCTGCGGCTCTCCGCGCGCGGTGATCCGGCCCGGATCTCGCGGG 6517
QY 1281 AATGGGCTCTCTCGATGTAGATCT--GATCGCGCTTGTGGGCGGAGATGAGGCGCTT 1338
DB 6518 AATGGGCTCTCTCGATGTAGATCTGCGATCCGCGCTTGTGGGCGGAGATGAGGCGGCTT 6577
QY 1339 TAAATTTT--CGCATGCTAAACAAGATCAGAGAAGGCGGAAAGGCGACATGTTTATA 1397
DB 6578 TAAATTTTCCGCAATGCTAAACAAGATCAGAGAAGGCGGAAAGGCGACATGTTTATA 6637
QY 1398 TTTTATATATTTCTGCTGCTGCTCGTCAGGCTTAGATGTGATCTTTCTTCTCT 1457
DB 6638 TTTTATATATTTCTGCTGCT--TCGTCAAGCTTAGATGTGATCTTTCTTCTCT 6695
QY 1458 TTTTGTGGTAGAATTTGAATCCCTCAGATTGTCATGCGTAGTCTTTTCATGAT 1517
DB 6696 TTTTGTGGTAGAATTTGAATCCCTCAGATTGTCATGCGTAGTCTTTTCATGAT 6755
QY 1518 TTTGTGCAAAATGAGCTCGTGGGAGCTTTTGTAGGTAGACCATG 1565
DB 6756 TTTGTGCAAAATGAGCTCGTGGGAGCTTTTGTAGGTAGACCATG 6803
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RESULT 13
US-09-845-064-21
/ Sequence 21, Application US/09845064
/ Publication No. US20030175976A1
/ GENERAL INFORMATION:
/ APPLICANT: MERISTEM THERAPEUTICS
/ TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS
/ TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR
/ TITLE OF INVENTION: METHODS OF PRODUCTION
/ FILE REFERENCE: SynVec1
/ CURRENT APPLICATION NUMBER: US/09/845,064
/ NUMBER OF SEQ. ID NOS: 57
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 21
/ LENGTH: 10003
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
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/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:Plasmid
/ OTHER INFORMATION: pMR1210
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/ FEATURE:
/ NAME/KEY: rep_origin
/ LOCATION: (1)..(654)
/ OTHER INFORMATION: Origin of replication ori RK2
/
/ FEATURE:
/ NAME/KEY: rep_origin
/ LOCATION: (655)..(1263)
/ OTHER INFORMATION: Origin of replication ori ColEI
/
/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (1264)..(2603)
/ OTHER INFORMATION: NPT III gene coding for neomycin
/ OTHER INFORMATION: phosphotransferase and kanamycin resistance
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (2604)..(4098)
/ OTHER INFORMATION: TrfA locus from RK2 coding for two proteins, P285
/ OTHER INFORMATION: and P382, enabling the increase of the replication
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (4106)..(4271)
/ OTHER INFORMATION: T-DNA left border
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/ FEATURE:
/ NAME/KEY: terminator
/ LOCATION: (4272)..(4559)
/ OTHER INFORMATION: No. US20030175976AlaIaline synthetase terminator
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/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (4559)..(4572)
/ OTHER INFORMATION: MCS multiple cloning site
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/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (4594)..(5169)
/ OTHER INFORMATION: Bar gene coding for phosphinothricine
/ OTHER INFORMATION: acetyltransferase and glutosinate resistance
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/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: (5170)..(5704)
/ OTHER INFORMATION: Rice Actin Intron
/
/ FEATURE:
/ NAME/KEY: promoter
/ LOCATION: (5705)..(6638)
/ OTHER INFORMATION: Rice Actin Promoter
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/ FEATURE:
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/ FEATURE:
/ NAME/KEY: misc_feature
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/ NAME/KEY: polyA signal
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/ OTHER INFORMATION: First exon-intron combination from Ubi-maize
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/ NAME/KEY: gene
/ LOCATION: (8085)..(9119)
/ OTHER INFORMATION: Hygromycin resistance gene from Escherichia coli
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/ NAME/KEY: promoter
/ LOCATION: (2941)..(4920)
/ OTHER INFORMATION: Ubi-promoter from maize
US-10-344-977A-1
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Query Match          24.6%; Score 384.8; DB 21; Length 9359;
Best Local Similarity 87.0%; Pred. No. 3.8e-79;
Matches 494; Conservative 0; Mismatches 62; Indels 12; Gaps 6;

QY 1004 CCACGCTGCCACCACTCCGCGTCTCCGCGCCAGACCAAGAAATTGGCCGACCG 1063
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DB 7527 CAACCTACCAACCAACCAACCACTCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 7586

QY 1064 CGGTGAGGCTCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1123
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DB 7587 AGCTCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 7645

QY 1124 CTTCTCTTCTCCGTTTTTTTTTTCGTCGCTCGATCTTGGCCTTGGTAGTTGGGT 1183
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DB 7646 CTTCTCTTCTCCGTTTTTTTTTTCGTCGCTCGATCTTGGCCTTGGTAGTTGGGT 7705

QY 1184 GGGCGAGA---CGGCTTGTGCGCCCAATCGGTGCGCGCGAGGCGGAGTCTCGCG 1239
    |||||
DB 7706 GGGCGAGAGCGGCTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 7765

QY 1240 CTGGCGCTCTCG--GGCGTAGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1297
    |||||
DB 7766 CTGGCGCTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 7825

QY 1298 TAGATCT--GATCCGCGCTGTGTGGGGAGATGATGGGCGTTTAAATTT--CGCATGC 1354
    |||||
DB 7826 TAGATCTGGGATCGCGCGCTGTGTGGGGAGATGATGGGCGTTTAAATTTCCGCATGC 7885

QY 1355 TAAACAAGATCAGAGAGAGGGGAAAAGGCACTATGTTATATTTTATATATTTCTGC 1414
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DB 7886 TAAACAAGATCAGAGAGAGGGGAAAAGGCACTATGTTATATTTTATATATTTCTGC 7945

QY 1415 TGCTGCTCGTCAAGCTTAGATGATCTTCTTCTCTTTTGGGTAGAAATT 1474
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DB 7946 TGCT--TCGTCAGGCTTAGATGATCTTCTTCTTCTTGTGGGTAGAAATT 8003

QY 1475 GAATCCCTCAGATTTGATCGGTAGTTTCTTTTCATGATTTGACAAATGACGCC 1534
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DB 8004 GAATCCCTCAGATTTGATCGGTAGTTTCTTTTCATGATTTGACAAATGACGCC 8063

QY 1535 TCGTGGAGACTTTTGTAGTAGACC 1562
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DB 8064 TCGTGGAGACTTTTGTAGTAGACC 8091
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Search completed: September 12, 2005, 09:26:03  
Job time : 1995.88 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 04:01:02 : Search time 5357.74 Seconds  
(without alignments)  
14153.802 Million cell updates/sec

Title: US-10-758-799-3

Perfect score: 1565

Sequence: 1 GAATTCCTGACGATCGACG.....TTTTTGTAGTAGACCAATG 1565

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

GenBank: \*  
1: gb\_ha: \*  
2: gb\_hg: \*  
3: gb\_in: \*  
4: gb\_cm: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1565	100.0	1565	6 A94725	A94725 Sequence 3
2	1565	100.0	1565	6 AR559745	AR559745 Sequence
3	1565	100.0	1565	6 BD128391	BD128391 Corn H3C4
4	1021	65.2	1021	6 A94723	A94723 Sequence 1
5	1021	65.2	1021	6 AR559743	AR559743 Sequence
6	1021	65.2	1021	6 BD128389	BD128389 Corn H3C4
7	454	29.0	454	6 A94724	A94724 Sequence 2
8	454	29.0	454	6 AR559744	AR559744 Sequence
9	454	29.0	454	6 BD128390	BD128390 Corn H3C4
10	400	25.6	1264	6 MZEH3C4	MZEH3C4 Maize (Zea
11	296	18.9	623	6 AX467609	AX467609 Sequence
12	296	18.9	623	8 OSACT1	OSACT1 O. sativa Ac
13	296	18.9	1392	6 IS0114	IS0114 Sequence 6
14	296	18.9	1404	6 IS0115	IS0115 Sequence 6
15	296	18.9	2199	6 IS0113	IS0113 Sequence 5
16	296	18.9	5643	6 IS0112	IS0112 Sequence 4
17	294	18.8	470	6 AX555357	AX555357 Sequence
18	237	15.1	4895	12 AY452735	AY452735 Reporter
19	236	15.1	1266	8 S44221	S44221 Act1=actin

20	236	15.1	4412	12 EVCOR112N	Z29587 Expression
21	236	15.1	4433	12 EVCOR11AN	Z29588 Expression
22	236	15.1	4486	12 EVCOR116N	Z29589 Expression
23	210	13.4	1121	6 AX641982	AX641982 Sequence
24	145	9.3	4032	6 A71435	A71435 Sequence 5
25	145	9.3	4032	6 AR207453	AR207453 Sequence
26	145	9.3	4032	6 AR564463	AR564463 Sequence
27	145	9.3	4032	6 BD065509	BD065509 Improved
28	145	9.3	7545	6 AX840288	AX840288 Sequence
29	145	9.3	7943	6 AX093010	AX093010 Sequence
30	145	9.3	9143	6 AX093007	AX093007 Sequence
31	145	9.3	10003	6 AX093016	AX093016 Sequence
32	145	9.3	11643	6 AX840289	AX840289 Sequence
33	142	9.1	9359	6 AX384394	AX384394 Sequence
34	142	9.1	9359	6 AX473364	AX473364 Sequence
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36	141	9.0	6865	6 AX093008	AX093008 Sequence
37	141	9.0	10003	6 AX093016	AX093016 Sequence
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39	141	9.0	13485	12 AY225220	AY225220 Cloning v
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41	140	8.9	3039	6 AR271022	AR271022 Sequence
42	140	8.9	3044	6 AR271033	AR271033 Sequence
43	140	8.9	3450	6 AR271020	AR271020 Sequence
44	140	8.9	3455	6 AR271032	AR271032 Sequence
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ALIGNMENTS

RESULT 1	A94725	Sequence 3 from Patent WO9934005.	DNA	linear	PAT 26-JAN-2000
LOCUS	A94725	Sequence 3 from Patent WO9934005.	DNA	linear	PAT 26-JAN-2000
DEFINITION	A94725	Sequence 3 from Patent WO9934005.	DNA	linear	PAT 26-JAN-2000
ACCESSION	A94725	Sequence 3 from Patent WO9934005.	DNA	linear	PAT 26-JAN-2000
VERSION	A94725.1	GI:6778990	DNA	linear	PAT 26-JAN-2000
KEYWORDS			DNA	linear	PAT 26-JAN-2000
SOURCE			DNA	linear	PAT 26-JAN-2000
ORGANISM			DNA	linear	PAT 26-JAN-2000
REFERENCE			DNA	linear	PAT 26-JAN-2000
AUTHORS			DNA	linear	PAT 26-JAN-2000
TITLE			DNA	linear	PAT 26-JAN-2000
JOURNAL			DNA	linear	PAT 26-JAN-2000
FEATURES			DNA	linear	PAT 26-JAN-2000
source			DNA	linear	PAT 26-JAN-2000
ORIGIN			DNA	linear	PAT 26-JAN-2000
promoter			DNA	linear	PAT 26-JAN-2000
intron			DNA	linear	PAT 26-JAN-2000
Query Match			DNA	linear	PAT 26-JAN-2000
Best Local Similarity			DNA	linear	PAT 26-JAN-2000
Matches 1565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			DNA	linear	PAT 26-JAN-2000
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DB	61	TTAATGAATGACCAATTTCTTATTAATCTTATTAACATTAATCTGTTTAAAT	120		
QY	121	TCAGTCTCAACATTCATTTCTTATTAATCTTATTAACATTAATCTGTTTAAAT	180		
DB	121	TCAGTCTCAACATTCATTTCTTATTAATCTTATTAACATTAATCTGTTTAAAT	180		
QY	181	TTCTTCATATTTTTTTTCTTATTAACATTTTGGGCTTACATCATCATATATCA	240		



Db	181	TTCTGCAATATTTTTCCTTAACAAATTTGGGCTTAAATTCATCATCTAATCA	240
OY	241	TCCTTCCGGGTGCTCTTAAAGATTCATCCTCTGAATCTTAATTCCTCAATAAGT	300
Db	241	TCCTTCCGGGTGCTCTTAAAGATTCATCCTCTGAATCTTAATTCCTCAATAAGT	300
OY	301	TCTCTAAATCAAGTCTCTAATAAGCAATCTAATATTAGAGCAATTTTATTTTGTAC	360
Db	301	TCTCTAAATCAAGTCTCTAATAAGCAATCTAATATTAGAGCAATTTTATTTTGTAC	360
OY	361	ATPACATATTGTCAACACTCTCAATAGCATTTTATGTATTTACTAATACCGATAT	420
Db	361	ATPACATATTGTCAACACTCTCAATAGCATTTTATGTATTTACTAATACCGATAT	420
OY	421	TTAAAGTATTCAAACGATGGAAGACTTTTATTAATTTATATTATAGAAATCCAGT	480
Db	421	TTAAAGTATTCAAACGATGGAAGACTTTTATTAATTTATATTATAGAAATCCAGT	480
OY	481	AGCGTTCCTAATATTAGATGATTTATTAGAGAGCGCTGTAGAAAACGTAAAAATCT	540
Db	481	AGCGTTCCTAATATTAGATGATTTATTAGAGAGCGCTGTAGAAAACGTAAAAATCT	540
OY	541	TTGATATTATTAATTAGAGTAGAGTAGCCTTATGCTTTPATAGATCTTTGATGAGCA	600
Db	541	TTGATATTATTAATTAGAGTAGAGTAGCCTTATGCTTTPATAGATCTTTGATGAGCA	600
OY	601	GCCTTATACGGTATATTTTTCGGATTTGGCGCTCTCATATTTTCACTCAAGCGCCCAATTT	660
Db	601	GCCTTATACGGTATATTTTTCGGATTTGGCGCTCTCATATTTTCACTCAAGCGCCCAATTT	660
OY	661	TCAGGTTTTCACCGAAGCGCCAGCTCTCTAACCACAAATTTGATACGTTGGCGGGTT	720
Db	661	TCAGGTTTTCACCGAAGCGCCAGCTCTCTAACCACAAATTTGATACGTTGGCGGGTT	720
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Db	721	TTCAAAAAGATCGGAAACCAATCTGACCCACCGCATGTAGGGCCCTGGATTCCTCCCTG	780
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Db	781	ATTATAGTCTTAGCCAAATAGAGACCAGAACCAACCATCAGCGGATCGTCCCTAGCTTC	840
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Db	841	CACCTCATCGGGCGGTCATCTCATCAACACTTATTCGGTAACTTGGCCATCTCC	900
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Db	901	GAAAAAATTCCTCGGCTCGCGCTCGCACCTCTAATAATPACCAATCCATACAGACGAT	960
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Db	1021	CGCGGTCTCTCGCGCGCAAGCAACAAAGAAATTGGCGGCACCGCGGTGAGACTCTCC	1080
OY	1081	CTTCCCTCTCGCGCGCGCGGTAAACAACCGCCCTCTCTCTTTCTCGGTTT	1140
Db	1081	CTTCCCTCTCGCGCGCGCGGTAAACAACCGCCCTCTCTCTTTCTCGGTTT	1140
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Db	1261	CGGCCCGGATTCCTGGCGGGGAAATGGGGCTCGCGATGTAGATCTGATCCCGTGTTCG	1320
Qy	1321	GGGAGATGATGGGGCGTTTAAATTTGGCATGCTAAACAAGATCAGAGAGGGGAAA	1380
Db	1321	GGGAGATGATGGGGCGTTTAAATTTGGCATGCTAAACAAGATCAGAGAGGGGAAA	1380
Qy	1381	GGGACATAAGTATTATATTTTTATATATTTCTGCTGCGCTCGTCAGGCTTAGATGCT	1440
Db	1381	GGGACATAAGTATTATATTTTTATATATTTCTGCTGCGCTCGTCAGGCTTAGATGCT	1440
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Db	1441	AGATCTTCTCTTCTCTCTTTTGTGGGTAGAATTTGAATTCCTCAGCATTTGTTACCGTA	1500
Qy	1501	GTTTTTCTTTTCATGATTTGTGACAAATGCAGCCTCGTGGAGCTTTTTTGTAGTAGA	1560
Db	1501	GTTTTTCTTTTCATGATTTGTGACAAATGCAGCCTCGTGGAGCTTTTTTGTAGTAGA	1560
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DEFINITION	AR559745		
ACCESSION	AR559745.1	GI:53969843	
VERSION			
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1565)		
TITLE	Derose, R. and Freysine, G.		
JOURNAL	Maize H3G4 promoter combined with the first intron of rice actin,		
FEATURES	Patent: US 6750378-A 3 15-JUN-2004;		
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Qy	121	TCAGTCTCAACATTCATTTGCTCAAGATAAGTTGAGACTGTCAAAATTTACTATTTAT	180
Db	121	TCAGTCTCAACATTCATTTGCTCAAGATAAGTTGAGACTGTCAAAATTTACTATTTAT	180
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Db	181	TTCTTCATATTTTTTTTCTTATACACATTTTGGGCTTACAAATCCATCATCTATATCCA	240
Qy	241	TCCTTCGCGGTGCTCTTAAAGATTCATCTCGAATCTTATTTCTCTCAATACGT	300
Db	241	TCCTTCGCGGTGCTCTTAAAGATTCATCTCGAATCTTATTTCTCTCAATACGT	300
Qy	301	TCTCTAAATCAGGCTCTTATAAGCAATACCTATATTAGACATTTTTTATTTTTTGAC	360
Db	301	TCTCTAAATCAGGCTCTTATAAGCAATACCTATATTAGACATTTTTTATTTTTTGAC	360
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Db      781 ATTAAGTCTTAGCCAAATAGAGGCCAGAAACCAACCATCAACGCGATGCTCTTACGCTTC 840
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RESULT 3
BD128391
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 1565)
Durose, R. and Freysset, G.
Corn H3c4 promoter bonded to the first intron of rice actin,
chimeric gene containing this promoter and transgenic plant
Patent: JP 200250016-A/3 08-JAN-2002;
AVENTIS CROPS/SCIENCE SA
OS Unidentified
PN JP 200250016-A/3
PF 08-JAN-2002
PR 22-DEC-1998 JP 2000526660
PR 24-DEC-1997 FR 97/16726
PI RICHARD DUROSE, GEORGES FREYSSET
PC C12N15/09, A01H5/00, C07K14/21, C07K14/415, C07K19/00, C12N5/10, PC
C1201/68
PC C12N15/00, C12N5/00
CC Strandedness: Single;
CC Topology: Linear;
CC Corn H3c4 promoter bonded to the first intron of rice actin,
CC containing this promoter and transgenic plant FH Key
CC Location/Qualifiers
FT source 1..1565
FEATURES
source 1..1565
Location/Qualifiers
1..1565
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/db_xref="taxon:32644"

ORIGIN
Query Match 100.0%; Score 1565; DB 6; Length 1565;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1565; Conservative 0;

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Db      241 TCGTTTCGGGTGTCCTAAAGATTCACCTCGTGAATCTTATCTCTCCAAATACGT 300
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Db      301 TCTCTAAATCAGGTCCTATATAGCAATACCTATATTAAGACATTTTTTATTTTGTAC 360
Qy      361 ATACATATTTGTATCTCTCAATGATATATACATATTTAGTTTACTAAACCGATAT 420
Db      361 ATACATATTTGTATCTCTCAATGATATATACATATTTAGTTTACTAAACCGATAT 420
Qy      421 TTAAGTATTCAAACGATGAAGACTGTTTATTAATTAATTTATATATAGAAATCAGT 480
Db      421 TTAAGTATTCAAACGATGAAGACTGTTTATTAATTAATTTATATATAGAAATCAGT 480
Qy      481 AGCGTTCTCTAAATTTTATGATGATTTATTAAGAGACGCTGTAGAAAAAGTAAATCT 540
Db      481 AGCGTTCTCTAAATTTTATGATGATTTATTAAGAGACGCTGTAGAAAAAGTAAATCT 540
Qy      541 TTGATTAATTTATTTATGAGGTAGATAGCTTATGCTTATATGATCTTTGGTGAACCA 600
Db      541 TTGATTAATTTATTTATGAGGTAGATAGCTTATGCTTATATGATCTTTGGTGAACCA 600
Qy      601 GCCTTATACCGGTTATTTTCGCGATTGCGCTCTCATTTTCACTCGAGCGCCACATTT 660
Db      601 GCCTTATACCGGTTATTTTCGCGATTGCGCTCTCTCATTTTCACTCGAGCGCCACATTT 660
Qy      661 TCACGTTTTTCAACGAAGCGCCGCTGCTTAACCAAAATTTGATAGCGTGGCGGTT 720
Db      661 TCACGTTTTTCAACGAAGCGCCGCTGCTTAACCAAAATTTGATAGCGTGGCGGTT 720
Qy      721 TTCAAAAGAAGTGGAAACCATCTGACCCACGACATAGAGGCGCTCGGATCTCCCTG 780
Db      721 TTCAAAAGAAGTGGAAACCATCTGACCCACGACATAGAGGCGCTCGGATCTCCCTG 780
Qy      781 ATTAAGTCTTAGCCAAATAGAGGCCAGAACCAACCATACGCGGATCTCTACGCTTC 840
Db      781 ATTAAGTCTTAGCCAAATAGAGGCCAGAACCAACCATACGCGGATCTCTACGCTTC 840
Qy      841 CACTCATACGCGCGCGCTCCATCTCCATCCAAACCTATTCGTTACTTTGCCATCTCC 900
Db      841 CACTCATACGCGCGCGCTCCATCTCCATCCAAACCTATTCGTTACTTTGCCATCTCC 900
Qy      901 GAAAAAATTCCTGGGCTCGCGCTCGGACCTACTACAAATACCATCCATCCACAGCAT 960
Db      901 GAAAAAATTCCTGGGCTCGCGCTCGGACCTACTACAAATACCATCCATCCACAGCAT 960
Qy      961 CGCATCACTGCAAAATCCCCCAAGAAATCAACACTTCCCAATTCACGCTGCCACAAC 1020
Db      961 CGCATCACTGCAAAATCCCCCAAGAAATCAACACTTCCCAATTCACGCTGCCACAAC 1020
Qy      1021 CGCGCTCTCCGCGCCCAAGACCAAAAGAAATGGCGCGCACCGCGGTGAGCTCTCC 1080
Db      1021 CGCGCTCTCCGCGCCCAAGACCAAAAGAAATGGCGCGCACCGCGGTGAGCTCTCC 1080
Qy      1081 CCGCGGCTCTCCGCGCCCAAGACCAAAAGAAATGGCGCGCACCGCGGTGAGCTCTCC 1140
Db      1081 CCGCGGCTCTCCGCGCCCAAGACCAAAAGAAATGGCGCGCACCGCGGTGAGCTCTCC 1140
Qy      1141 TTTTTCGTCCTCGGTCCTCATCTTTGGCTTTGGATGTTGGGTGGGCGAAGCGGCTTC 1200
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Qy      1201 TCGCCCAAGATCGGTGCGCGGAGGAGCGGATCTCGCGCTGAGCTCCGGCGTGAAGT 1260
Db      1201 TCGCCCAAGATCGGTGCGCGGAGGAGCGGATCTCGCGCTGAGCTCCGGCGTGAAGT 1260
Qy      1261 CGGCGCGGATCTCGCGGAGGAGGAGGCTCGCGATGATAGATCGGCGCTGAGTGG 1320
Db      1261 CGGCGCGGATCTCGCGGAGGAGGAGGCTCGCGATGATAGATCGGCGCTGAGTGG 1320
Qy      1321 GGGAGATGATGGGCGCTTTAAATTTTCGCATGCTAAACAAATCAGAGAGAGGAGAAA 1380

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Db      1321 GGGAGATGATGGGCGCTTTAAATTTCCCATGCTAAACAAATCAGAGAGAGGAGAAA 1380
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Db      1381 GGGCACTATGGTTATATTTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1440
Qy      1441 AGATCTTTCTTTCTTTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCATTTGTCAGGTA 1500
Db      1441 AGATCTTTCTTTCTTTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCATTTGTCAGGTA 1500
Qy      1501 GTTTTCTTTTATATGATTTTGACAAATGACAGCCCTGCGGAGAGCTTTTGTAGTGA 1560
Db      1501 GTTTTCTTTTATGATTTTGACAAATGACAGCCCTGCGGAGAGCTTTTGTAGTGA 1560
Qy      1561 CCATG 1565
Db      1561 CCATG 1565

RESULT 4
A94723
LOCUS      A94723      1021 bp      DNA      linear      PAT 26-JAN-2000
DEFINITION Sequence 1 from Patent W0934005.
ACCESSION A94723
VERSION    A94723.1 GI:6778988
KEYWORDS
SOURCE     unidentified
           unidentified
           unclassified.
REFERENCE 1 (bases 1 to 1021)
AUTHORS   Derose,R. and Freysinet,G.
TITLE      MAIZE H3CA PROMOTER ASSOCIATED WITH FIRST RICE ACTIN INTRON,
           CHIMERIC GENE CONTAINING IT AND TRANSFORMED PLANT
JOURNAL    Patent: WO 934005-A 1 08-JUL-1999;
           RHONE-POULENC AGROCHIMIE (FR)
FEATURES
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                   /organism="unidentified"
                   /mol_type="unassigned DNA"
                   /db_xref="taxon:32644"
                   Location/Qualifiers
ORIGIN
Promoter
Query Match      65.2%; Score 1021; DB 6; Length 1021;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1021; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      361 CATTATACATATTTAGTTTACTAAACCGATTAATTAAAGTATTCAAAGCATGAAGAAC 420
QY      447 TGTTTAGATTAATTTCTATATATATAGAGATCCAGTACGGTCTCTAAATTTAGATGATAT 506
Db      421 TGTATGATTAATTTCTATATATATAGAGATCCAGTACGGTCTCTAAATTTAGATGATAT 480
QY      507 TTGAGAGACGCTGTATGAAAACGTAAAAATCTTTGATTAATTATTTAGAGGTAGAT 566
Db      481 TTGAGAGACGCTGTATGAAAACGTAAAAATCTTTGATTAATTATTTAGAGGTAGAT 540
QY      567 AGCTTTATGCTTTATATAGATCTTTGATGAGACCGACTTATACGGTATTTTCGCGAT 626
Db      541 AGCTTTATGCTTTATATAGATCTTTGATGAGACCGACTTATACGGTATTTTCGCGAT 600
QY      627 GCGCTCTCATTTTCACTCCAGCGCCCAATTTTCAAGTTTTCACGAAACGCCGCCAGCC 686
Db      601 GCGCTCTCATTTTCACTCCAGCGCCCAATTTTCAAGTTTTCACGAAACGCCGCCAGCC 660
QY      687 TGCCTAACCAAAATTTGTAAGGTGGCGGGGTTTTCAAAAGAAAGTCGGAACATCTGC 746
Db      661 TGCCTAACCAAAATTTGTAAGGTGGCGGGGTTTTCAAAAGAAAGTCGGAACATCTGC 720
QY      747 ACCACCGACTAGTAGGCGCTCGGATCTCTCGATTAAGTCTTACGCAATAGAGGCCA 806
Db      721 ACCACCGACTAGTAGGCGCTCGGATCTCTCGATTAAGTCTTACGCAATAGAGGCCA 780
QY      807 GAAACACCCATCAACGCGGATCGTCCCTTCCATTCACCTCATCGCGCGCTTCATCTCA 866
Db      781 GAAACACCCATCAACGCGGATCGTCCCTTCCATTCACCTCATCGCGCGCTTCATCTCA 840
QY      867 TCCAAACACTTATTCCTTACCTTGGCCATCTCTCGAAAAAATTCCTCGGCTCGGCTCCG 926
Db      841 TCCAAACACTTATTCCTTACCTTGGCCATCTCTCGAAAAAATTCCTCGGCTCGGCTCCG 900
QY      927 ACCCTACGAAATATACCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCAT 986
Db      901 ACCCTACGAAATATACCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCAT 960
QY      987 ATCAACACTTCCCAATTCACGCTGCCACCAACTCGCGCTCTCCGCGCCAGACCAAA 1046
Db      961 ATCAACACTTCCCAATTCACGCTGCCACCAACTCGCGCTCTCCGCGCCAGACCAAA 1020
QY      1047 G 1047
Db      1021 G 1021

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RESULT 5
LOCUS   AR559743                      1021 bp    DNA      linear    PAT 08-OCT-2004
DEFINITION
ACCESSION AR559743
VERSION   AR559743.1 GI:53969841
KEYWORDS
SOURCE    Unknown.
           Unclassified.
REFERENCE
  1 (bases 1 to 1021)
  Derose R. and Freyresinet G.
  Maize H3c4 promoter combined with the first intron of rice actin,
  chimeric gene compilising it and transformed plant
  Patent: US 6750378-A 1 15-JUN-2004;
  Location/Qualifiers
    1..1021
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ORIGIN
Query Match      65.2%; Score 1021; DB 6; Length 1021;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1021; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      27 CTATATGCAACATTTACTGTAATGCAATATCATTTTAATGAATAGCAAACTTTCTATT 86

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Db      1 CTTATGTGACCACTTTACTGTAATGCAATATCATTTTAATGAATAGCAAACTTTCTATT 60
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Db      61 ACTTCTTTAATAATTTGTTTAAATTCAGTCTTCAATTCATTCATTCGCAAG 120
QY      147 TATTAAGTGAACCTGCAAAATTTACTATTTTCTCATATTTTCTTCTTCTTCTTCTTCTTCT 206
Db      121 TATTAAGTGAACCTGCAAAATTTACTATTTTCTCATATTTTCTTCTTCTTCTTCTTCTTCT 180
QY      207 CATTTTGGCCTTACATCATCATCATATATATCATCATCTTTCGAGTCTCTTCTTCTTCTTCTTCT 266
Db      181 CATTTTGGCCTTACATCATCATCATATATATCATCATCTTTCGAGTCTCTTCTTCTTCTTCTTCT 240
QY      267 CCATCTCTGAAATCTTATTCCTCTCGAATPACGTTCTCTAATACAGTCTCTATTAAGCA 326
Db      241 CCATCTCTGAAATCTTATTCCTCTCGAATPACGTTCTCTAATACAGTCTCTATTAAGCA 300
QY      327 TACCTATATTAAGACATTTTATTTTATTTTGTATACATATTTTGTATATCTCTCAATG 386
Db      301 TACCTATATTAAGACATTTTATTTTATTTTGTATACATATTTTGTATATCTCTCAATG 360
QY      387 CATTATACATATTTAGTTTATTTTACCTAACCGATTAATTAAAGTATTCAAACGATGAAGAAC 446
Db      361 CATTATACATATTTAGTTTATTTTACCTAACCGATTAATTAAAGTATTCAAACGATGAAGAAC 420
QY      447 TGTTTAGATTAATTTCTATATATAGAGATCCAGTACGGTCTCTTAAATTTAGATGATAT 506
Db      421 TGTTTAGATTAATTTCTATATATAGAGATCCAGTACGGTCTCTTAAATTTAGATGATAT 480
QY      507 TTGAGAGACGCTGTATGAAAACGTAAAAATCTTTGATTAATTATTTAGAGGTAGAT 566
Db      481 TTGAGAGACGCTGTATGAAAACGTAAAAATCTTTGATTAATTATTTAGAGGTAGAT 540
QY      567 AGCTTTATGCTTTATATAGATCTTTGATGAGACCGACTTATACGGTATTTTCGCGAT 626
Db      541 AGCTTTATGCTTTATATAGATCTTTGATGAGACCGACTTATACGGTATTTTCGCGAT 600
QY      627 GCGCTCTCATTTTCACTCCAGCGCCCAATTTTCAAGTTTTCACGAAACGCCGCCAGCC 686
Db      601 GCGCTCTCATTTTCACTCCAGCGCCCAATTTTCAAGTTTTCACGAAACGCCGCCAGCC 660
QY      687 TGCCTAACCAAAATTTGTAAGGTGGCGGGTTCAAAAGAAAGTCGGAACATCTGC 746
Db      661 TGCCTAACCAAAATTTGTAAGGTGGCGGGTTCAAAAGAAAGTCGGAACATCTGC 720
QY      747 ACCACCGACTAGTAGGCGCTCGGATCTCTCGATTAAGTCTTACGCAATAGAGGCCA 806
Db      721 ACCACCGACTAGTAGGCGCTCGGATCTCTCGATTAAGTCTTACGCAATAGAGGCCA 780
QY      807 GAAACACCCATCAACGCGGATCGTCCCTTCCATTCACCTCATCGCGCGCTTCATCTCA 866
Db      781 GAAACACCCATCAACGCGGATCGTCCCTTCCATTCACCTCATCGCGCGCTTCATCTCA 840
QY      867 TCCAAACACTTATTCCTTACCTTGGCCATCTCTCGAAAAAATTCCTCGGCTCGGCTCCG 926
Db      841 TCCAAACACTTATTCCTTACCTTGGCCATCTCTCGAAAAAATTCCTCGGCTCGGCTCCG 900
QY      927 ACCCTACGAAATATACCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCAT 986
Db      901 ACCCTACGAAATATACCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCAT 960
QY      987 ATCAACACTTCCCAATTCACGCTGCCACCAACTCGCGCTCTCCGCGCCAGACCAAA 1046
Db      961 ATCAACACTTCCCAATTCACGCTGCCACCAACTCGCGCTCTCCGCGCCAGACCAAA 1020
QY      1047 G 1047
Db      1021 G 1021

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RESULT 6

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BD128389  
LOCUS BD128389 1021 bp DNA linear PAT 18-SEP-2002  
DEFINITION Corn H3C4 promoter bonded to the first intron of rice actin,  
chimeric gene containing this promoter and transgenic plant.  
ACCESSION BD128389  
VERSION BD128389.1 GI:23223334  
KEYWORDS JP 200250016-A/1.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 1021)  
AUTHORS Durose,R. and Freysinet,G.  
TITLE Corn H3C4 promoter bonded to the first intron of rice actin,  
chimeric gene containing this promoter and transgenic plant  
JOURNAL Patent: JP 200250016-A 1 08-JAN-2002;  
COMMENT AVENTIS CROPS/SCIENCE SA  
OS Unidentified  
PN JP 200250016-A/1  
PD 08-JAN-2002  
PF 22-DEC-1998 JP 2000526660  
PI 24-DEC-1997 FR 97/16726  
PR RICHARD DUROSE,GEORGES,FREYSINET  
PC C12N15/09,A01H5/00,C07K14/21,C07K14/415,C07K19/00,C12N5/10,PC  
C12Q1/68,  
PC C12N15/00,C12N5/00  
CC Strandedness: Single;  
CC Topology: linear;  
CC Corn H3C4 promoter bonded to the first intron of rice actin,  
CC chimeric gene  
CC containing this promoter and transgenic plant FH Key  
FT Location/Qualifiers  
FT source 1..1021  
1..1021 /organism='unidentified'.  
/mol\_type='genomic DNA'  
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Query Match 65.2%; Score 1021; DB 6; Length 1021;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1021; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 CTTATGTCACGCACTTACTGTGTAATGCAATATCAATTAATGAATAGCAACTTTTCATT 86  
DB 1 CTTATGTCACGCACTTACTGTGTAATGCAATATCAATTAATGAATAGCAACTTTTCATT 60  
QY 87 ACTTCTTTACTAATCAATATCTTGTTTAAATTCAGTCTGCAACATTCATTGCTCAAG 146  
DB 61 ACTTCTTTACTAATCAATATCTTGTTTAAATTCAGTCTGCAACATTCATTGCTCAAG 120  
QY 147 TATTAAGTGAAGCTGTCACAAATTTACTATTATTTCTTCATATTTTTTCTTATACA 206  
DB 121 TATTAAGTGAAGCTGTCACAAATTTACTATTATTTCTTCATATTTTTTCTTATACA 180  
QY 207 GATTTGGGCTTACCAATCATCATATATCATATCCATTCCTGCGTGCCTTAAAGATT 266  
DB 181 GATTTGGGCTTACCAATCATCATATATCCATTCCTTCCGATGCTCTTAAAGATT 240  
QY 267 CCATCCTCTGAAATCTTATCTCTCCAAATAGCTTCTTAAATCAGGTCCTTAAAGCA 326  
DB 241 CCATCCTCTGAAATCTTATCTCTCCAAATAGCTTCTTAAATCAGGTCCTTAAAGCA 300  
QY 327 TACCTATATTAGAGACATTTTTTATTTTTTGTACATACATATTGTCATACCTCAATG 386  
DB 301 TACCTATATTAGAGACATTTTTTATTTTTTGTACATACATATTGTCATACCTCAATG 360  
QY 387 CATTAATACATATTAGTTTACTAAACGATTTAAATTTAAATTTCAACGAGTGAAGAAC 446  
DB 361 CATTAATACATATTAGTTTACTAAACGATTTAAATTTAAATTTCAACGAGTGAAGAAC 420  
QY 447 TGTTAGATTAATTTCTATATATAGAGATCCAGTAGCGTTCTTAAATTTAGATGATTAT 506

DB 421 TGTTAGATTAATTTCTATATATAGAGATCCAGTAGCGTTCTTAAATTTAGATGATTAT 480  
QY 507 TTAGAGAGCGCGTTAGAAAAAGTAAAAATTTCTTTGATTTATTTATTTAGGGTAGAGT 566  
DB 481 TTAGAGAGCGCGTTAGAAAAAGTAAAAATTTCTTTGATTTATTTATTTAGGGTAGAGT 540  
QY 567 ACCCTTTATGCTTTTATAGATCTTTGTGTGAGACCCAGCTTATACCGTTATTTTCGCATT 626  
DB 541 AGCCTTTATGCTTTTATAGATCTTTGTGTGAGACCCAGCTTATACCGTTATTTTCGCATT 600  
QY 627 GCGCTCTCATTTTCACTTCACAGCGCCCAATTTACAGTTTTCACCGAGCGCCAGCC 686  
DB 601 GCGCTCTCATTTTCACTTCACAGCGCCCAATTTTCAGTTTTCACCGAGCGCCAGCC 660  
QY 687 TGCCCTAACCAAAATTTGTATCGGTGGGGGTTTTTCAAAAAGAAAGTCGAAACCATCTGC 746  
DB 661 TGCCCTAACCAAAATTTGTATCGGTGGGGGTTTTTCAAAAAGAAAGTCGAAACCATCTGC 720  
QY 747 ACCCAACCGACTAGTAGCGCTTCGATTCCTCCCTGATTAAGTCTTAGCCAAATAGAGCCCA 806  
DB 721 ACCCAACCGACTAGTAGCGCTTCGATTCCTCCCTGATTAAGTCTTAGCCAAATAGAGCCCA 780  
QY 807 GAACCAACCCATACGCGGATGCTCCCTTAGAGCTTCAACTCATCGCGCGCTCATCTCCA 866  
DB 781 GAACCAACCCATACGCGGATGCTCCCTTAGAGCTTCAACTCATCGCGCGCTCATCTCCA 840  
QY 867 TCCCAACCGCTATTCGGTTACCTTGCCTTCCTCCGAAATTTCTCGGCTCGCTCCGC 926  
DB 841 TCCCAACCGCTATTCGGTTACCTTGCCTTCCTCCGAAATTTCTCGGCTCGCTCCGC 900  
QY 927 ACTTACTCAAAATACCAATCCATCCATCAGACGATCGATCACTGTGCAATTCGCCAGAAA 986  
DB 901 ACTTACTCAAAATACCAATCCATCCATCAGACGATCGATCACTGTGCAATTCGCCAGAAA 960  
QY 987 ATCAACACTCCCAATTCACAGCTGTCACAACTGCGGCTCTCGCGCCGAAGCAACAAA 1046  
DB 961 ATCAACACTCCCAATTCACAGCTGTCACAACTGCGGCTCTCGCGCCGAAGCAACAAA 1020  
QY 1047 G 1047  
DB 1021 G 1021

RESULT 7  
A94724 454 bp DNA linear PAT 26-JAN-2000  
LOCUS A94724  
DEFINITION Sequence 2 from Patent WO934005.  
ACCESSION A94724  
VERSION A94724.1 GI:678989  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 454)  
AUTHORS Durose,R. and Freysinet,G.  
TITLE MAIZE H3C4 PROMOTER ASSOCIATED WITH FIRST RICE ACTIN INTRON,  
CHIMERIC GENE CONTAINING IT AND TRANSFORMED PLANT  
JOURNAL Patent: WO 934005-A 2 08-JUL-1993;  
Rhone Poulenc Agrochimie (FR)  
FEATURES  
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ORIGIN  
intron  
Query Match 29.0%; Score 454; DB 6; Length 454;  
Best Local Similarity 100.0%; Pred. No. 2e-238;  
Matches 454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1102 GTAACCAACCCCGCCCT 1161

Db	1	GTAAACACCCGCCCCCTCCCTCTTTCTTTCTCCGTTTTTTTTTTTCGTCCGTGGCTCGAT	60
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Db	61	CTTTGGCCTTGGTAGTTGGGTGGGCGAGAGCGCTTCGTGCCCAATCGGTGCGCGG	120
OY	1222	AGGGCGGGGAACTCCGCGGCTGGCGCTCCCGGCGTGAATCCGCGCCGGAATCCTCCGCGGGGA	1281
Db	121	AGGGCGGGGAACTCCGCGGCTGGCGCTCCCGGCGTGAATCCGCGCCGGAATCCTCCGCGGGGA	180
OY	1282	ATGGGCGCTCTCGGAGTGAATCTGAATCCGCGCTTTTGGGCGAGATGAATGGGCGCTTAA	1341
Db	181	ATGGGCGCTCTCGGAGTGAATCTGAATCCGCGCTTTTGGGCGAGATGAATGGGCGCTTAA	240
OY	1342	AATTTCCGCAATCTAAACAAGATCAGAGAGAGGGGAAAAAGGCACTAATGTTTAAATTTT	1401
Db	241	AATTTCCGCAATCTAAACAAGATCAGAGAGAGGGGAAAAAGGCACTAATGTTTAAATTTT	300
OY	1402	TATATATTTTCGTCTGCTGTCTGTCAAGGCTTGAATGTCTAATCTTTTCTTTCTTTT	1461
Db	301	TATATATTTTCGTCTGCTGTCTGTCAAGGCTTGAATGTCTAATCTTTTCTTTCTTTT	360
OY	1462	GTGGGTAAATTTGAATCCCTCAGATGTTCAATGGTATTTTCTTTATATGAATTTGT	1521
Db	361	GTGGGTAAATTTGAATCCCTCAGATGTTCAATGGTATTTTCTTTATATGAATTTGT	420
OY	1522	GACAATCAGAGCTGTGCGAGAGCTTTTTTTGTAG 1555	
Db	421	GACAAATCAGAGCTGTGCGAGAGCTTTTTTTGTAG 454	

RESULT	8
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DEFINITION	Sequence 2 from patent US 6750378.
ACCESSION	AR559744
VERSION	AR559744.1   GI:5369842
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 454)
TITLE	Derosc,R. and Freyssinet,G. Maize H3C4 promoter combined with the first intron of rice actin, chimeric gene comprising ic and transformed plant Patent: US 6750378-A 2 15-JUN-2004; Location/Qualifiers 1..454 /organism="unknown" /mol_type="genomic DNA"
JOURNAL FEATURES	
source	
ORIGIN	
Query Match	29.0% ; Score 454; DB 6; Length 454;
Beet Local Similarity	100.0%; Pred. No. 2e+238;
Matches 454; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1102 GTAAACCACCCCGCCCCCTCTCTCTTTCGTTTTTTTTCGTGGTGCATCAT 1161
Db	1 GTAACACACCCGCCCCCTCTCTCTTCTTCTCGTTTTTTTTCGTGGTGCATCAT 60
QY	1162 CTTTGAGCTTGAGTTTGAGTGAGTGAGAGAGCGAGCGCTTGCGCCCAAGATCGGTGCGCGGG 1221
Db	61 CTTTGAGCTTGAGTTTGAGTGAGTGAGAGAGAGCGAGCGCTTGCGCCCAAGATCGGTGCGCGGG 120
QY	1222 AGGGGCGGGATCTTCGCGGCTGGCGGTCTCCGGGCGTAGATCCGCGCCCGGAATCTTCGGGGGGA 1281
Db	121 ACGGGCGGGATCTTCGCGGCTGGCGGTCTCCGGGCGTAGATCCGCGCCCGGAATCTTCGGGGGGA 180
QY	1282 ATGGGGGCTTCGGAGTGTAGATCTGATCCGCGCGTTGTGGGGGAGAATGATGGGGCGTTTAA 1341
Db	181 ATGGGGGCTTCGGAGTGTAGATCTGATCCGCGCGTTGTGGGGGAGAATGATGGGGCGTTTAA 240

Accession	Sequence	Length
QY	1342 AATTTGGCAGTCGTAACACAGATCAGGAGAGGGGAAAAGGGCACTAGTTTAAATTT	1401
Db	241 AATTTGGCAGTCGTAACACAGATCAGGAGAGGGGAAAAGGGCACTAGTTTAAATTT	300
QY	1402 TAAATTAATTTCTGCTGCTGCTGCTGTCAGGCTTAGAGTGTGAATCTTTTCTTCTTTT	1461
Db	301 TAAATTAATTTCTGCTGCTGCTGCTGTCAGGCTTAGAGTGTGAATCTTTTCTTCTTTT	360
QY	1462 GTGGGTGAATTTGAATCCCTCAGCATTTGCATCCGGAGATTTTCTTTTCATGATTTGT	1521
Db	361 GTGGGTGAATTTGAATCCCTCAGCATTTGCATCCGGAGATTTTCTTTTCATGATTTGT	420
QY	1522 GACAAATGCAAGCTCTGTGCGGAGCTTTTGTAG	1555
Db	421 GACAAATGCAAGCTCTGTGCGGAGCTTTTGTAG	454

	RESULT 9	
BD128390	BD128390	454 bp DNA linear PAT 18-SEP-2007
DEFINITION	Corn H3C4 promoter bonded to the first intron of rice actin, chimeric gene containing this promoter and transgenic plant.	
ACCESSION	BD128390	
VERSION	BD128390.1 GI:23223335	
KEYWORDS	JP 2002500016-A/2.	
SOURCE	unidentified	
ORGANISM	unclassified.	
REFERENCE	1 (bases 1 to 454)	
AUTHORS	Durose,R. and Freyssi�r,G.	
TITLE	Corn H3C4 promoter bonded to the first intron of rice actin, chimeric gene containing this promoter and transgenic plant Patent; JP 2002500016-A 2 08-JAN-2002;	
JOURNAL	AVANTIS CROPS&SCIENCE SA	
COMMENT	OS Unidentified PN JP 2002500016-A/2 PD 08-JAN-2002 JP 2000526660 PF 22-DEC-1998 JP 2000526660 PR 24-DEC-1997 FR 97/16726 PI RICHARD DUROSE,GEORGES FREYSSI�R PC C12N15/09,A01H5/00,C07K14/21,C07K14/415,C07K19/00,C12N5/10, PC C12O1/66, PC C12N15/00,C12N5/00 CC Strandedness: Single; CC Topology: Linear; CC Corn H3C4 promoter bonded to the first intron of rice actin, chimeric gene CC containing this promoter and transgenic plant FH Key CC Location/Qualifiers FT source 1..454 FT /organism='Unidentified'.	
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ORIGIN		
Query Match	29.0%; Score 454; DB 6; Length 454;	
Best Local Similarity	100.0%; Prid. No. 2e-238;	
Matches	454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1102 GTAACACACCGGCCCTCCCTCTTCCTTCTTCGCGTTTCTTTTTTTCGTGCATCTGCAT	116
DB	1 GTAACACACCGGCCCTCCCTCTTCCTTCTTCGCGTTTCTTTTTTTCGTGCATCTGCAT	60
QY	1162 CT TTGGCCTTGTAAGTTGGTGGGCGAGACGGCTTCGTGCCCCAGATCGATGCGCGG	1221
DB	61 CT TTGGCCTTGTAAGTTGGTGGGCGAGACGGCTTCGTGCCCCAGATCGATGCGCGG	120
QY	1222 AGGGCGGGGAATCTCGCGGCTGGCGTCCTCCGGGCGTAGTGGGCCCGAATCTCTCGCGGGA	1289
DB	121 AGGGCGGGGAATCTCGCGGCTGGCGTCCTCCGGGCGTAGTGGGCCCGAATCTCTCGCGGGA	180

OY	1282	ATGGGGCTCTGGAGTGTGATCTGATCCGCCGTTGTTGGGGGAGATGATGGGGCGTTAA	1341
Db	181	ATGGGGCTCTGGAGTGTGATCTGATCCGCCGTTGTTGGGGGAGATGATGGGGCGTTAA	240
OY	1342	AATTTGCGCATGCTAAACAAAGATCAGGAAGAGGGGAAAAGGCACTATGTTTATATTTT	1401
Db	241	AATTTGCGCATGCTAAACAAAGATCAGGAAGAGGGGAAAAGGCACTATGTTTATATTTT	300
OY	1402	TATATATTTCTGCTGCTGCTGCTGACGGTTGTGATGCTATATCTTTCTTCTCTTTT	1461
Db	301	TATATATTTCTGCTGCTGCTGCTGACGGTTGTGATGCTATATCTTTCTTCTCTTTT	360
OY	1462	GTGGGTAGAAATTGATCCCTCAGCATTTTCATCGTAGTATTTTCTTTTCATGATTTGT	1521
Db	361	GTGGGTAGAAATTGATCCCTCAGCATTTTCATCGTAGTATTTTCTTTTCATGATTTGT	420
OY	1522	GACAAATGACGCTCTGCGGAGCTTTTGTAG	1555
Db	421	GACAAATGACGCTCTGCGGAGCTTTTGTAG	454

	RESULT 10			
LOCUS	MZEH3C4	1264 bp	DNA	linear PLN 27-APR-1993
DEFINITION	Maize (Zea mays) histone H3 gene (H3C4), complete cde.			
ACCESSION	M13379			
VERSION	M13379.1	GI:168496		
KEYWORDS	histone.			
SOURCE	Zea mays			
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogonaceae; Zea.			
REFERENCE	1 (bases 1 to 1264)			
AUTHORS	Chabuet,N., Phillips,G., Chabutou,M.-E., Ehling,M. and Giotoc,C.			
TITLE	Nucleotide sequences of the corn histone H3 and H4 genes organization of the corn histone H3 and H4 genes			
JOURNAL	Plant Mol. Biol. 6, 253-263 (1986).			
COMMENT	Original source text: Maize DNA, clone H3C4. Draft entry and printed copy of the sequence [1] kindly provided by C.Giotoc, 10-OCT-1986. Location/Qualifiers			
FEATURES				
Source	1..1264 /organism="Zea mays" /mol_type="Genomic DNA" /db_xref="taxon:4577" 526..936 /note="histone H3" /codon_start=1 /db_xref="GI:168497" /translat="MARTKOTARKSTGSKAEPKOLATWAKRSAPATGVKKPRFRRP GTVALREIRYOKSTELRIKLRFQRLVRELAOPFKDLRFQSAAVALGEAAEAAYIV GLFDPTNCAIHAKRVTIMPDIDQLARRIRERA"			
CDS				
ORIGIN	54 bp upstream of BglII site.			
	Query Match               25.6%; Score 400; DB 8; Length 1264; Best Local Similarity 100.0%; Pred. No. 1,4e-208; Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Oy	648 GCGCCCCCATTTTCAGTTCATTCCAGGAAGGCCCGACGGCTTAACAAGAATTGGTA 707			
Db	120 GCGCCCCCATTTTCACGTTTTACCGAAGCCCACCAGCTGCCTAACCACAAATGGTA 179			
Oy	708 CGTGCGCCGCGTTTTCAAGAAGTCGAAAAACATCTCACCCACCGACTAGTAGCCCT 767			
Db	180 CGTGCGCCGCGTTTTCAABAAGAATCGAANAACATCTGACCCACCGACTAGTAGCCCT 239			
Oy	768 CGAATCTTCCTCGATTAAAGTCTAGGCCAATAGAGCCCAAGAACCAACCATCAGCGGATC 827			
Db	240 CGAATCTTCCTCGATTAAAGTCTAGGCCAATAGAGCCCAAGAACCAACCATCAGCGGATC 299			

[illegible]

LOCUS	AX467609	623 bp	DNA	linear	PAT 16-JUL-2002
DEFINITION	Sequence 19 from Patent WO0234926.				
ACCESSION	AX467609				
VERSION	AX467609.1	GI:21900797			
KEYWORDS					
SOURCE	.				
ORGANISM	Oryza sativa				
	Oryza sativa				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.				
REFERENCE	1				
AUTHORS	Sticklen,M.B., Dale,B.E. and Magboo,J.S.				
TITLE	Transgenic plants containing ligninase and cellulase which degrade lignin and cellulose to fermentable sugars				
JOURNAL	Patent: WO 0234926-A 19 02-MAY-2002; MICHIGAN STATE UNIVERSITY (US)				
FEATURES	Location/Qualifiers				
source	1..623				
	/organism="Oryza sativa"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:4530"				
ORIGIN					
Query Match	18.9%; Score 296; DB 6; Length 623;				
Best Local Similarity	100.0%; Pred.No. 3.6e-151;				
Matches 296; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
QY	1265 CCGAGTCTCGCGGGGAATGGGGGCTCGCGATGTAGATCTGATCGCGCGTTGTTGGGGGA	1322			
DB	278 CCGAGTCTCGCGGGGAATGGGGGCTCTCGATGTAGATCTGATCGCGCGTTGTTGGGGGA	337			
QY	1325 GATGATGGGGCGTTTAAATTTGCGCATGCTAAACAGATCAGAAAGGGGAAAAGGCG	1388			
DB	338 GATGATGGGGCGTTTAAATTTGCGCATGCTAAACAGATCAGAAAGGGGAAAAGGCG	397			
QY	1385 ACTATGTTTATATTTATATATTTCTGCGTGCCTGCTGAGGGTTTATGATGTCTAGT	1444			
DB	398 ACTATGTTTATATTTATATATTTCTGCGTGCCTGCTGAGGGTTTATGATGTCTAGT	457			
QY	1445 CTTCCTTCTCTTTTGTGGGTAGAAATTGATCCCTCAGCATTTGTCATCGTAGTTT	1504			
DB	458 CTTCCTTCTCTTTTGTGGGTAGAAATTGATCCCTCAGCATTTGTCATCGTAGTTT	517			
QY	1505 TTCTTTTATGATTTTGACAAATGACACCTCGTGGGAGCTTTTGTAGGTAGA	1560			
DB	518 TTCTTTTATGATTTTGACAAATGACACCTCGTGGGAGCTTTTGTAGGTAGA	573			
RESULT 12					
OSACT1					
LOCUS	OSACT1	623 bp	DNA	linear	PLN 24-MAR-1997
DEFINITION	O.sativa Act1 gene.				
ACCESSION	X63830				
VERSION	X63830.1	GI:468505			









GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 03:55:48 ; Search time 896.833 Seconds  
(without alignments)  
10330.128 Million cell updates/sec

Title: US-10-758-799-3

Perfect score: 1565  
Sequence: 1 GAATTCCTGACAGTCACAGG.....TTTTTGTAGTACACCATG 1565

Scoring table: OLIGO\_NUC  
Gapop\_60.0, Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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13: geneseq2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1565	100.0	1565	2	AAZ91039
2	1021	65.2	1021	2	AAZ91037
3	454	29.0	454	2	AAZ91038
4	296	18.9	623	3	AAZ47117
5	296	18.9	623	6	ABK6738
6	296	18.9	1392	2	AAT80053
7	296	18.9	2199	2	AAT80052
8	296	18.9	5643	2	AAT80055
9	294	18.8	470	6	ABT07357
10	294	18.8	470	10	ADF49181
11	236	15.1	1259	6	ADG69912
12	236	15.1	1259	11	ADN88926
13	236	15.1	3657	6	ADG69892
14	236	15.1	4604	6	ADG69905
15	236	15.1	4773	6	ADG69901
16	236	15.1	4773	11	ADN88915
17	236	15.1	4950	6	ADG69903
18	236	15.1	4950	11	ADN88917
19	236	15.1	4965	6	ADG69906
20	236	15.1	4974	6	ADG69904

21	236	15.1	4974	11	ADN88918	Adn88918 pU04 vect
22	236	15.1	5164	11	ADN88919	Adn88919 pP010.1 v
23	236	15.1	5267	11	ADN88907	Adn88907 pTP8-5 ve
24	236	15.1	5277	6	ADG69894	Adg69894 Vector pT
25	236	15.1	5277	11	ADN88909	Adn88909 pTP5-1 ve
26	236	15.1	5295	6	ADG69907	Adg69907 Vector pU
27	236	15.1	5295	11	ADN88922	Adn88922 pUG4 vect
28	236	15.1	5327	6	ADG69896	Adg69896 Vector pT
29	236	15.1	5327	11	ADN88911	Adn88911 pTP42 ve
30	236	15.1	5337	6	ADG69888	Adg69888 Vector pU
31	236	15.1	5337	6	ADG69900	Adg69900 Vector pT
32	236	15.1	5337	11	ADN88914	Adn88914 pTP5 vect
33	236	15.1	5337	11	ADN88903	Adn88903 pTP4 vect
34	236	15.1	5338	6	ADG69884	Adg69884 Vector pT
35	236	15.1	5338	6	ADG69898	Adg69898 Vector pT
36	236	15.1	5338	11	ADN88913	Adn88913 pTP3-1 ve
37	236	15.1	5338	11	ADN88899	Adn88899 pTP10-1 v
38	236	15.1	5345	6	ADG69886	Adg69886 Vector pU
39	236	15.1	5345	11	ADN88901	Adn88901 pU4-4 ve
40	236	15.1	5387	6	ADG69910	Adg69910 Vector pT
41	236	15.1	5387	11	ADN88925	Adn88925 pTP11-1 v
42	236	15.1	5395	6	ADG69890	Adg69890 Vector pT
43	236	15.1	5395	11	ADN88905	Adn88905 pTP5.14 v
44	236	15.1	5510	2	AA012707	Aag12707 Rice acti
45	236	15.1	5595	11	ADN88920	Adn88920 pU03 vect

## ALIGNMENTS

RESULT 1	
AAZ91039	AAZ91039 standard; DNA; 1565 BP.
ID	
XX	
AC	AAZ91039;
XX	
DT	17-OCT-2003 (revised)
DT	06-JUN-2000 (first entry)
XX	
DE	Chimeric maize H3C4 promoter/rice actin gene intron 1 regulatory region.
XX	
KW	Regulatory element; monocotyledonous vegetable plant cell; maize;
KW	histone H3C4; promoter; rice actin gene intron; chimeric; ss;
KW	herbicide resistance.
OS	Zea mays.
OS	Oryza sativa.
OS	Chimeric.
PN	FR2772787-A1.
PD	25-JUN-1999.
XX	
PF	24-DEC-1997; 97FR-00016726.
XX	
PR	24-DEC-1997; 97FR-00016726.
XX	
PA	(RHON ) RHONE-POULENC AGROCHIMIE.
XX	
PI	Derose R, Freysinet G;
XX	
DR	WPI; 1999-397352/34.
PT	5' chimeric regulatory region comprising maize histone H3C4 promoter and
PT	rice actin gene first intron.
XX	
PS	Claim 8; Page 15-16; 24pp; French.
CC	The invention relates to a DNA sequence comprising a 5' regulatory
CC	element for the expression of a heterologous gene in a monocotyledonous
CC	vegetable plant cell. The DNA (this sequence) comprises: (a) a functional
CC	fragment of the maize histone H3C4 promoter sequence (AAZ91037; and (b) a
CC	functional fragment of the first intron of the rice actin gene

CC (AA291038) . The chimeric regulatory region is useful for the expression of heterologous genes that confer resistance to certain herbicides, or that have novel agronomical properties in monocotyledons. In particular, the chimeric 5' regulatory gene is linked to an enzyme that confers resistance to a specific herbicide. This is useful for controlling weeds in fields of plants/grains that have been transformed with the chimeric gene. The herbicide can be applied to the field without affecting the plant/grain. (Updated on 17-Oct-2003 to standardise OS field)

XX Sequence 1565 BP; 366 A; 415 C; 297 G; 487 T; 0 U; 0 Other;

Query Match 100.0%; Score 1565; DB 2; Length 1565;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GAATTCCTGACGATCGACGATCCCTTATGTCACCAATTAATGATATCAT 60
DB 1 GAATTCCTGACGATCGACGATCCCTTATGTCACCAATTAATGATATCAT 60
QY 61 TTAATGGAATAGCAAACTTTTCTATTACTCTTACCAATTAATGATATTA 120
DB 61 TTAATGGAATAGCAAACTTTTCTATTACTCTTACCAATTAATGATATTA 120
QY 121 TCAAGTCTCAACATTCATGCTCAAGTATTAAGTGAAGTCAAAATTTA 180
DB 121 TCAAGTCTCAACATTCATGCTCAAGTATTAAGTGAAGTCAAAATTTA 180
QY 181 TTCTTCAATTTTTCCTTATACACATTTGGGCTTACATCATCATATTC 240
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DB 361 ATATCATATTTGTCATCTCAAAATGATATTAATTTAGTTTACCAAC 420
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QY 601 GCGTTATACCGGTTATTTGCGATGCGCTCTCATTTTACATCCAGCC 660
DB 601 GCGTTATACCGGTTATTTGCGATGCGCTCTCATTTTACATCCAGCC 660
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QY 721 TTCAAAAGAAATGGAACATCTGCAACCAAGACTAGTAGAGCCCT 780
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QY 781 ATTAAGCTTAGGCAATAGAGCCGCAACCAACCAATGAGGATGTCCT 840
DB 781 ATTAAGCTTAGGCAATAGAGCCGCAACCAACCAATGAGGATGTCCT 840
QY 841 CACCTCATCGGCGCGCTCATCTCCATCAACACTATTCGTTACCTTCC 900
DB 841 CACCTCATCGGCGCGCTCATCTCCATCAACACTATTCGTTACCTTCC 900

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DB 841 CACCTCATCGGCGCGCTCATCTCCATCAACACTATTCGTTACCTTCC 900
QY 901 GAAAAAATTTTCGCTCGCGCTCCGACCTTACCAATATCCATCCATCA 960
DB 901 GAAAAAATTTTCGCTCGCGCTCCGACCTTACCAATATCCATCCATCA 960
QY 961 CGCATCTAGTCCAAATCCCGCAAGAAATCAACACTCCCAATTCAG 1020
DB 961 CGCATCTAGTCCAAATCCCGCAAGAAATCAACACTCCCAATTCAG 1020
QY 1021 CGCGTCTCTCGCGCGCAACCAAGAAATTTGCGCGCACCGCGTGA 1080
DB 1021 CGCGTCTCTCGCGCGCAACCAAGAAATTTGCGCGCACCGCGTGA 1080
QY 1081 CCTCCCGCTCGCGCGCGCGGTAAACACCCCGCTCTCTCTTTCTTC 1140
DB 1081 CCTCCCGCTCGCGCGCGCGGTAAACACCCCGCTCTCTCTTTCTTC 1140
QY 1141 TTTTTCGCTCTCGATCTCGATCTTTGACCTTGTGATGTTGAGAG 1200
DB 1141 TTTTTCGCTCTCGATCTCGATCTTTGACCTTGTGATGTTGAGAG 1200
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DB 1201 TCGCCCAATGCTGCTCGCGCGGAGGAGGAGTCTCGCGCGTGA 1260
QY 1261 CGGCGCGGATCTCTCGCGGAGGAGGAGTCTCGCGCGTGA 1320
DB 1261 CGGCGCGGATCTCTCGCGGAGGAGGAGTCTCGCGCGTGA 1320
QY 1321 GGGAGATGATGAGGAGGATTTAAATTTGCGATGCTAAACAGATCA 1380
DB 1321 GGGAGATGATGAGGAGGATTTAAATTTGCGATGCTAAACAGATCA 1380
QY 1381 GGGCACTATGTTTATTTTATTTATTTTCTGCTGCTGCTGCTGCT 1440
DB 1381 GGGCACTATGTTTATTTTATTTTATTTTCTGCTGCTGCTGCTGCT 1440
QY 1441 AGATCTTCTCTCTCTTTTGTGGTAGAAATTTGAATCCCTCAGAT 1500
DB 1441 AGATCTTCTCTCTCTTTTGTGGTAGAAATTTGAATCCCTCAGAT 1500
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DB 1501 GTTTTCTTTTATGATTTTGAACAAATGACGCTGTCGAGGCTTT 1560
QY 1561 CCATG 1565
DB 1561 CCATG 1565

RESULT 2
AA291037
ID AA291037 standard; DNA; 1021 BP.
XX
XX AA291037;
AC
XX
XX 06-JUN-2000 (first entry)
DT
XX
XX Maize histone H3C4 promoter region.
DE
XX
XX Regulatory element; monocotyledonous vegetable plant cell; maize;
KW histone H3C4; promoter; rice actin gene intron; chimeric; ss;
KW herbicide resistance.
OS
XX
XX Zea mays.
XX
XX FR2772787-A1.
PN
XX
XX 25-JUN-1999.
PD
XX
XX 24-DEC-1997; 97PR-00016726.
PF
XX
XX

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PR 24-DEC-1997; 97FR-00016726.  
 XX (RHON ) RHONE-POULENC AGROCHIMIE.  
 XX Derose R, Freyssinet G;  
 XX WPI, 1999-397352/34.  
 DR 5' chimeric regulatory region comprising maize histone H3C4 promoter and  
 PT rice actin gene first intron.  
 XX  
 PS Claim 3; Page 13; 24pp; French.  
 CC The invention relates to a DNA sequence (AA291039) comprising a 5'  
 CC regulatory element for the expression of a heterologous gene in a  
 CC monocotyledonous vegetable plant cell. The DNA comprises: (a) a  
 CC functional fragment of the maize histone H3C4 promoter sequence (this  
 CC sequence); and (b) a functional fragment of the first intron of the rice  
 CC actin gene (AA291038). The chimeric regulatory region is useful for the  
 CC expression of heterologous genes that confer resistance to certain  
 CC herbicides, or that have novel agronomical properties in monocotyledons.  
 CC In particular, the chimeric 5' regulatory gene is linked to an enzyme  
 CC that confers resistance to a specific herbicide. This is useful for  
 CC controlling weeds in fields of plants/grains that have been transformed  
 CC with the chimeric gene. The herbicide can be applied to the field without  
 CC affecting the plant/grain  
 XX  
 SQ Sequence 1021 BP; 283 A; 275 C; 140 G; 323 T; 0 U; 0 Other;

Query Match 65.2%; Score 1021; DB 2; Length 1021;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1021; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 CTTATGTCACCAATTTCTGTAATGCAATTCATTTATGTAAGCAAACTTTCTATT 86  
 DB 1 CTTATGTCACCAATTTCTGTAATGCAATTCATTTATGTAAGCAAACTTTCTATT 60  
 QY 87 ACTTCTTACTTAACATTAATCTTGTTTAAATTCAGTCCCTCAACTTCATTCGCTCAG 146  
 DB 61 ACTTCTTACTTAACATTAATCTTGTTTAAATTCAGTCCCTCAACTTCATTCGCTCAG 120  
 QY 147 TATTAAGTGAACCTGTGTAATTTTACATTTTATTTCTCATTTTCTTCTTACACA 206  
 DB 121 TATTAAGTGAACCTGTGTAATTTTACATTTTATTTCTCATTTTCTTCTTACACA 180  
 QY 207 CATTGTCGCTTCAACATTCATTCATTCATTCCTTCCGCTGCTCTTAAAGATT 266  
 DB 181 CATTGTCGCTTCAACATTCATTCATTCATTCCTTCCGCTGCTCTTAAAGATT 240  
 QY 267 CCAATCCTGTAATCTTATCTCTCAATAACGTTCTTAATCAGGTCCTTAAGCAA 326  
 DB 241 CCAATCCTGTAATCTTATCTCTCAATAACGTTCTTAATCAGGTCCTTAAGCAA 300  
 QY 327 TACCTAATTAAGACATTTTATTTTGTACATACATTTTGTATATCTGCAATG 386  
 DB 301 TACCTAATTAAGACATTTTATTTTGTACATACATTTTGTATATCTGCAATG 360  
 QY 387 CATTATCATATTTAGTTTACTTAACCGATTATTTAAAGATTCAACGAGTAAGAAC 446  
 DB 361 CATTATCATATTTAGTTTACTTAACCGATTATTTAAAGATTCAACGAGTAAGAAC 420  
 QY 447 TGTTTAGATTAATCTTATATATAGAAATCCAGTAGCGTCTTAAATTTAGATGATAT 506  
 DB 421 TGTTTAGATTAATCTTATATATAGAAATCCAGTAGCGTCTTAAATTTAGATGATAT 480  
 QY 507 TTAGAAGACGCTGTAGAAAACGTAATAATCTTTGATATTTATTTTAAAGGTAGAGT 566  
 DB 481 TTAGAAGACGCTGTAGAAAACGTAATAATCTTTGATATTTATTTTAAAGGTAGAGT 540  
 QY 567 AGCCTTATGCTTATATAGATCTTTGTGAGCCAGCCTTATACCGGTTATTTTGCAGAT 626  
 DB 541 AGCCTTATGCTTATATAGATCTTTGTGAGCCAGCCTTATACCGGTTATTTTGCAGAT 600

QY 627 GGCCCTCTGATTTTCACTCCAGGCGCCCAATTTTCAAGCTTTTACAGGAAGGCCAGCC 686  
 DB 601 GGCCCTCTGATTTTCACTCCAGGCGCCCAATTTTCAAGCTTTTACAGGAAGGCCAGCC 660  
 QY 687 TGCCTAACCAACAAATTTGCTAGCGTGGCGCGGTTTCAAAAGAGTGGAAACCATCTGC 746  
 DB 661 TGCCTAACCAACAAATTTGCTAGCGTGGCGCGGTTTCAAAAGAGTGGAAACCATCTGC 720  
 QY 747 ACCCAGCGACTAGTAGGCGCTTGGGATCTTCCTGATTAAGTCTTACCAATAGAGCCCA 806  
 DB 721 ACCCAGCGACTAGTAGGCGCTTGGGATCTTCCTGATTAAGTCTTACCAATAGAGCCCA 780  
 QY 807 GAACCAACCATCAACGGGATTCGCTTACGCTTCCACTATGCGGCGCTTCATCCCA 866  
 DB 781 GAACCAACCATCAACGGGATTCGCTTACGCTTCCACTATGCGGCGCTTCATCCCA 840  
 QY 867 TCCAAACCTAATTCCTTACCTTCCATCTTCCGAAATTTCTGCGCTCGGCTCCGC 926  
 DB 841 TCCAAACCTAATTCCTTACCTTCCATCTTCCGAAATTTCTGCGCTCGGCTCCGC 900  
 QY 927 ACCTACTCAAAATACCATTCCTCAACGACATCGCATCTGCAAAATCCCGAGAAA 986  
 DB 901 ACCTACTCAAAATACCATTCCTCAACGACATCGCATCTGCAAAATCCCGAGAAA 960  
 QY 987 ATCAACACCTCCCAATTTCCACGCTGCAACCACTGCGGCTCCGCGCAAGCAACAA 1046  
 DB 961 ATCAACACCTCCCAATTTCCACGCTGCAACCACTGCGGCTCCGCGCAAGCAACAA 1020  
 QY 1047 G 1047  
 DB 1021 G 1021

RESULT 3  
 ID AA291038 standard; DNA; 454 BP.  
 XX AA291038;  
 AC 06-JUN-2000 (first entry)  
 DT XX  
 DE Rice actin gene intron 1 sequence.  
 XX  
 KW Regulatory element; monocotyledonous vegetable plant cell; maize;  
 KM histone H3C4; promoter; rice actin gene intron; chimeric; ss;  
 XX herbicide resistance.  
 OS Oryza sativa.  
 XX  
 PN FR272787-A1.  
 XX  
 PD 25-JUN-1999.  
 XX  
 PF 24-DEC-1997; 97FR-00016726.  
 XX  
 PR 24-DEC-1997; 97FR-00016726.  
 XX  
 PA (RHON ) RHONE-POULENC AGROCHIMIE.  
 XX  
 PI Derose R, Freyssinet G;  
 XX  
 DR WPI, 1999-397352/34.  
 XX  
 PT 5' chimeric regulatory region comprising maize histone H3C4 promoter and  
 PT rice actin gene first intron.  
 PS Claim 5; Page 14; 24pp; French.  
 XX  
 CC The invention relates to a DNA sequence (AA291039) comprising a 5'  
 CC regulatory element for the expression of a heterologous gene in a  
 CC monocotyledonous vegetable plant cell. The DNA comprises: (a) a  
 CC functional fragment of the maize histone H3C4 promoter sequence  
 CC (AA291037); and (b) a functional fragment of the first intron of the rice





Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1265 CCGGATCCTCGGGGGAATGGGCTCTCGGATGATGATCGATCCGCCGTTGTGGGGGA 1324  
 DB 1076 CCGGATCCTCGGGGGAATGGGCTCTCGGATGATGATCGATCCGCCGTTGTGGGGGA 1135

QY 1325 GATGATGGGCGCTTTAAATTTGCCATGCTAAACAGATCAGAAAGAGGGGAAAAGGCG 1384  
 DB 1136 GATGATGGGCGCTTTAAATTTGCCATGCTAAACAGATCAGAAAGAGGGGAAAAGGCG 1195

QY 1385 ACTATGTTTATATTTTATATATTTCTGCTGCTCGTCAAGCTTATGATGTCTAGAT 1444  
 DB 1196 ACTATGTTTATATTTTATATATTTCTGCTGCTCGTCAAGCTTATGATGTCTAGAT 1255

QY 1445 CTTTCCTTCTCTTTTGTGGGTAATTTGAATCCCTCGCATGTGTCAATGGTGTGT 1504  
 DB 1256 CTTTCCTTCTCTTTTGTGGGTAATTTGAATCCCTCGCATGTGTCAATGGTGTGT 1315

QY 1505 TTCTTTTCATGATTTTGTGACAAATGCAGCCTCGTGGGAGCTTTTGTAGTAGA 1560  
 DB 1316 TTCTTTTCATGATTTTGTGACAAATGCAGCCTCGTGGGAGCTTTTGTAGTAGA 1371

RESULT 7  
 AAT80052  
 ID AAT80052 standard; cDNA; 2199 BP.  
 XX  
 AC AAT80052;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 04-NOV-1997 (first entry)  
 XX  
 DE Rice actin 1 gene promoter region.  
 XX  
 KM Promoter; rice; actin 1 gene; cytoplasm; cytoskeleton; extension growth;  
 KM cytoplasmic streaming; cell division; Rac1; maize; Adh1 promoter; ss.  
 XX  
 OS Oryza sativa.  
 OS  
 PN US5641876-A.  
 XX  
 PD 24-JUN-1997.  
 XX  
 PF 27-OCT-1993; 93US-00144602.  
 XX  
 PR 05-JAN-1990; 90US-00461490.  
 PR 18-SEP-1991; 91US-00762680.  
 XX  
 PA (CORR ) CORNELL RES FOUND INC.  
 PA  
 PI Wu R, McElroy D;  
 XX  
 DR WPI; 1997-340996/31.  
 XX  
 PT Nucleic acid containing the promoter of the rice actin-1 gene - used to  
 PT direct efficient expression of foreign genes in rice.  
 XX  
 PS Claim 3; Col 33-36; 29pp; English.  
 PS  
 XX This sequence represents the promoter region from the rice actin-1 (Rac1)  
 CC gene. Cytoplasmic actin is a fundamental and essential component of the  
 CC eukaryotic cell and cytoskeleton. In higher plant cells, a number of  
 CC cellular processes, such as cytoplasmic streaming, extension growth and  
 CC cell division are thought to involve the cytoskeletal actin protein. All  
 CC of the studied plant actins consist of four exons of conserved length,  
 CC separated by 3 introns of variable length. In rice there are at least 8  
 CC actin-like sequences per haploid genome. Rac1 encodes a transcript that  
 CC is relatively abundant in all rice tissues. This sequence is an example  
 CC of a nucleic acid molecule of the invention. The nucleic acid molecules  
 CC of the invention contain the Rac1 gene (or fragments) with promoter  
 CC activity in monocotyledonous plants. The promoter is used to direct  
 CC expression of foreign genes in transgenic rice and other plants. The  
 CC actin promoter is more efficient in rice transformation than previously

CC proposed promoters (e.g. 5 times more active than the maize Adh1  
 CC promoter) and has constitutive activity in space and time. (Updated on 25  
 CC -MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 2199 BP; 603 A; 515 C; 446 G; 635 T; 0 U; 0 Other;

Query Match 18.9%; Score 296; DB 2; Length 2199;  
 Best Local Similarity 100.0%; Pred. No. 6e-130;  
 Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1265 CCGGATCCTCGGGGGAATGGGCTCTCGGATGATGATCGATCCGCCGTTGTGGGGGA 1324  
 DB 1883 CCGGATCCTCGGGGGAATGGGCTCTCGGATGATGATCGATCCGCCGTTGTGGGGGA 1942

QY 1325 GATGATGGGCGCTTTAAATTTGCCATGCTAAACAGATCAGAAAGAGGGGAAAAGGCG 1384  
 DB 1943 GATGATGGGCGCTTTAAATTTGCCATGCTAAACAGATCAGAAAGAGGGGAAAAGGCG 2002

QY 1385 ACTATGTTTATATTTTATATATTTCTGCTGCTCGTCAAGCTTATGATGTCTAGAT 1444  
 DB 2003 ACTATGTTTATATTTTATATATTTCTGCTGCTCGTCAAGCTTATGATGTCTAGAT 2062

QY 1445 CTTTCCTTCTCTTTTGTGGGTAATTTGAATCCCTCGCATGTGTCAATGGTGTGT 1504  
 DB 2063 CTTTCCTTCTCTTTTGTGGGTAATTTGAATCCCTCGCATGTGTCAATGGTGTGT 2122

QY 1505 TTCTTTTCATGATTTTGTGACAAATGCAGCCTCGTGGGAGCTTTTGTAGTAGA 1560  
 DB 2123 TTCTTTTCATGATTTTGTGACAAATGCAGCCTCGTGGGAGCTTTTGTAGTAGA 2178

RESULT 8  
 AAT80055  
 ID AAT80055 standard; cDNA; 5643 BP.  
 XX  
 AC AAT80055;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 04-NOV-1997 (first entry)  
 XX  
 DE Rice actin 1 gene.  
 XX  
 KM Promoter; rice; actin 1 gene; cytoplasm; cytoskeleton; extension growth;  
 KM cytoplasmic streaming; cell division; Rac1; maize; Adh1 promoter; ss.  
 XX  
 OS Oryza sativa.  
 OS  
 PN US5641876-A.  
 XX  
 PD 24-JUN-1997.  
 XX  
 PF 27-OCT-1993; 93US-00144602.  
 XX  
 PR 05-JAN-1990; 90US-00461490.  
 PR 18-SEP-1991; 91US-00762680.  
 XX  
 PA (CORR ) CORNELL RES FOUND INC.  
 PA  
 PI Wu R, McElroy D;  
 XX  
 DR WPI; 1997-340996/31.  
 XX  
 PT Nucleic acid containing the promoter of the rice actin-1 gene - used to  
 PT direct efficient expression of foreign genes in rice.  
 XX  
 PS Example 1; Col 3-7; 29pp; English.  
 PS  
 XX This sequence represents a the rice actin-1 (Rac1) gene amplified using  
 CC AAT80054. Cytoplasmic actin is a fundamental and essential component of  
 CC the eukaryotic cell and cytoskeleton. In higher plant cells, a number of  
 CC cellular processes, such as cytoplasmic streaming, extension growth and  
 CC cell division are thought to involve the cytoskeletal actin protein. All  
 CC of the studied plant actins consist of four exons of conserved length,

CC separated by 3 introns of variable length. In rice there are at least 8  
CC actin-like sequences per haploid genome. Ractl encodes a transcript that  
CC is relatively abundant in all rice tissues. This sequence is an example  
CC of a nucleic acid molecule of the invention. The nucleic acid molecule  
CC of the invention contains the Ractl gene, or fragments with promoter  
CC activity (see AAT80052 and AAT80053) in monocotyledonous plants. The  
CC promoter is used to direct expression of foreign genes in transgenic rice  
CC and other plants. The actin promoter is more efficient in rice  
CC transformation than previously proposed promoters (e.g. 5 times more  
CC active than the maize Adh1 promoter) and has constitutive activity in  
CC space and time. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 5643 BP; 1500 A; 1283 C; 1200 G; 1660 T; 0 U; 0 Other;

Query Match 18.9%; Score 296; DB 2; Length 5643;  
Best Local Similarity 100.0%; Pred. No. 5,9e-130;  
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1265 CCGGATCTCGCGGGAATGGGCTCTCGATGTGATGATCCGCCGTTGTTGGGGGA 1324  
DB 1886 CCGGATCTCGCGGGAATGGGCTCTCGATGTGATGATCCGCCGTTGTTGGGGGA 1945  
QY 1325 GATGATGGGCGTTAAATTTCCCATGCTAAACAAGATCAGGAAGGGGAAAAAGGCG 1384  
DB 1946 GATGATGGGCGTTAAATTTCCCATGCTAAACAAGATCAGGAAGGGGAAAAAGGCG 2005  
QY 1385 ACTATGGTTATATTTTATATATTTCTGCTGCTGCTGCTAGAGCTTAGATGTCTAGAT 1444  
DB 2006 ACTATGGTTATATTTTATATATTTCTGCTGCTGCTGCTAGAGCTTAGATGTCTAGAT 2065  
QY 1445 CTTTCTTCTCTTTTGTGGGTAGATTTGAAATCCCTCAGCATTTGTCATCGTACTTT 1504  
DB 2066 CTTTCTTCTCTTTTGTGGGTAGATTTGAAATCCCTCAGCATTTGTCATCGTACTTT 2125  
QY 1505 TTCTTTTCATGATTTTGACAAATGCAAGCTCGTGGGAGCTTTTGTAGGTAGA 1560  
DB 2126 TTCTTTTCATGATTTTGACAAATGCAAGCTCGTGGGAGCTTTTGTAGGTAGA 2181

## RESULT 9

ID ABT07357 standard; DNA; 470 BP.  
XX ABT07357;  
AC ABT07357;  
XX 07-NOV-2002 (first entry)  
XX Reporter construct fragment rice actin intron SEQ ID NO: 109.  
DE  
XX Plant; gene expression control; insect; hormone receptor; fertility;  
KM ecdysone receptor; ds.  
XX Oryza sativa.  
OS  
XX MO200261102-A2.  
PN  
XX 08-AUG-2002.  
PD  
XX 24-OCT-2001; 2001WO-US051417.  
PF  
XX 24-OCT-2000; 2000US-0242969P.  
PR  
XX (SYGN) SYNGENTA PARTICIPATIONS AG.  
PA  
XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;  
PI WPI; 2002-619259/66.  
XX  
XX New receptor cassette encoding a chimeric receptor polypeptide, useful in  
PT regulating expression of target polypeptides in plants in the presence of  
XX appropriate ligands that may be used in controlling plant fertility.  
PS Example 10; Page 263; 319pp; English.

XX The present invention relates to a receptor cassette encoding a chimeric  
CC receptor polypeptide comprising at least one DNA binding domain, a hinge  
CC domain of an ecdysone receptor (ECR) of an insect, a ligand binding  
CC domain of an insect ECR, where the ligand binding domain is heterologous  
CC with respect to the hinge domain and an activation domain. The chimeric  
CC insect hormone receptors and receptor cassettes are useful in regulating  
CC expression of target polypeptides in plants in the presence of  
CC appropriate ligands that may be used in controlling plant fertility. The  
CC method is useful for decreasing or increasing plant gene expression. The  
CC present sequence is a polynucleotide described in the exemplification of  
CC the invention

XX Sequence 470 BP; 75 A; 103 C; 141 G; 151 T; 0 U; 0 Other;

Query Match 18.8%; Score 294; DB 6; Length 470;  
Best Local Similarity 100.0%; Pred. No. 5,6e-129;  
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1267 GGATCTCGCGGGAATGGGCTCTCGATGTGATGATCCGCCGTTGTTGGGGGA 1326  
DB 166 GGATCTCGCGGGAATGGGCTCTCGATGTGATGATCCGCCGTTGTTGGGGGA 225  
QY 1327 TGATGGGCGGTTAAATTTCCCATGCTAAACAAGATCAGGAAGGGGAAAAAGGCGAC 1386  
DB 226 TGATGGGCGGTTAAATTTCCCATGCTAAACAAGATCAGGAAGGGGAAAAAGGCGAC 285  
QY 1387 TATGTTTATATTTTATATATTTCTGCTGCTGCTGCTAGAGCTTAGATGTCTAGATCT 1446  
DB 286 TATGTTTATATTTTATATATTTCTGCTGCTGCTGCTAGAGCTTAGATGTCTAGATCT 345  
QY 1447 TTCTTTCTTCTTTTGTGGGTAGATTTGAAATCCCTCAGCATTTGTCATCGTACTTTT 1506  
DB 346 TTCTTTCTTCTTTTGTGGGTAGATTTGAAATCCCTCAGCATTTGTCATCGTACTTTT 405  
QY 1507 CTTTTCATGATTTTGACAAATGCAAGCTCGTGGGAGCTTTTGTAGGTAGA 1560  
DB 406 CTTTTCATGATTTTGACAAATGCAAGCTCGTGGGAGCTTTTGTAGGTAGA 459

## RESULT 10

ID ADF49181 standard; DNA; 470 BP.  
XX ADF49181;  
AC ADF49181;  
XX 12-FEB-2004 (first entry)  
XX Rice actin intron.  
DE  
XX  
XX receptor cassette; chimeric receptor polypeptide; DNA binding domain;  
KM hinge domain; ecdysone receptor; ECR; ligand binding domain;  
XX activation domain; transgenic seed; transgenic plant; plant line;  
KM herbicide; pesticide; rice; actin; intron; ds.  
XX  
XX Oryza sp.  
OS  
XX US2003154509-A1.  
PN  
XX 14-AUG-2003.  
PD  
XX 24-OCT-2001; 2001US-00087167.  
PF  
XX 24-OCT-2001; 2001US-00087167.  
PR  
XX 24-OCT-2001; 2001US-00087167.  
XX  
XX (PASC/) PASCAL E J.  
PA (VALE/) VALENTINE S A.  
PA (BROW/) BROWN J A.  
PA (COCK/) COCKRELL A S.  
PA (JOHN/) JOHNSON B D.  
XX  
XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;  
PI







XX (GEMV ) GENENCOR INT INC.  
PA Dunn-Coleman N, Langdon T, Morris P;  
XX WPI; 2003-457563/43.  
XX  
XX New transgenic plant comprising an expression cassette with a promoter  
PT operably linked to a ferulic acid esterase encoding polynucleotide, useful  
PT for enhancing availability of fermentable carbohydrates as feed for grass  
PT -fed animals.  
XX  
XX Disclosure; Fig 50; 190pp; English.  
XX  
XX The present invention relates to transgenic plants comprising an  
CC expression cassette having a promoter operably linked to a ferulic acid  
CC esterase (FAE) encoding polynucleotide. The transgenic plants are useful  
CC for enhancing the availability of fermentable carbohydrates as feed for  
CC grass-fed animals. The methods are useful for reducing the levels of  
CC phenolic acids in the cell walls available for cross-linking either by  
CC directly disrupting ester bonds linking phenolics and lignins to cell  
CC wall polysaccharides or by preventing excessive fermentation of cell wall  
CC carbohydrates. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 1259 BP; 337 A; 332 C; 268 G; 322 T; 0 U; 0 Other;  
  
Query Match 15.1%; Score 236; DB 11; Length 1259;  
Best Local Similarity 100.0%; Pred. No. 2e-101;  
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1069 GAGCTCTCCCTCCCTCCCTCCGCGCGCGGTACACCCCGCTCTCTCTTC 1128  
Db GAGCTCTCTCCCTCCCTCCCTCCGCGCGCGGTACACCCCGCTCTCTCTTC 955  
QY 1129 TTTCTCCGTTTTTTTTTGTGCTCGATCTTTGGCTTGTGATTTGGGTGGCG 1188  
Db TTTCTCCGTTTTTTTTTGTGCTCGATCTTTGGCTTGTGATTTGGGTGGCG 1015  
QY 1189 AGAGCGGCTTGTGCGCCAGATCGTGCGCGAGGCGGAGATCTCGCGCTGCGCTCT 1248  
Db 1016 AGAGCGGCTTGTGCGCCAGATCGTGCGCGAGGCGGAGATCTCGCGCTGCGCTCT 1075  
QY 1249 CCGGCGCTGAGTGCGCGCGGATCTCGCGGGAATGGGGCTCTCGAGTGTAGATCT 1304  
Db 1076 CCGGCGCTGAGTGCGCGCGGATCTCGCGGGAATGGGGCTCTCGAGTGTAGATCT 1131  
  
RESULT 13  
ADG69892  
ID ADG69892 standard; DNA; 3657 BP.  
XX  
AC ADG69892;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Vector pTP8-5 nucleotide sequence.  
XX  
DE transgenic plant; ferulic acid esterase; FAE; enzyme; phenolic acid;  
KM plant; cell wall; improved digestibility; biomass conversion;  
KM highly fermentable carbohydrate; gene; ds.  
XX  
OS Synthetic.  
XX  
PN WO200268666-A1.  
XX  
PD 06-SEP-2002.  
XX  
PF 16-NOV-2001; 2001WO-US043588.  
XX  
PR 17-NOV-2000; 2000US-0249608P.  
XX  
PA (GEMV ) GENENCOR INT INC.

PI Dunn-Coleman N, Langdon T, Morris P;  
XX WPI; 2002-698675/75.  
DR P-PSDB; ADG69893.  
XX  
XX New transgenic plant comprising an expression cassette with a promoter  
PT operably linked to a ferulic acid esterase encoding polynucleotide,  
PT useful in improving digestibility for livestock and enhancing biomass  
PT conversion.  
XX  
XX Disclosure; Fig 36B-E; 208pp; English.  
XX  
XX The present invention describes a transgenic plant (I) comprising an  
CC expression cassette with a promoter operably linked to a ferulic acid  
CC esterase encoding polynucleotide. Also described: (1) controlling (M1)  
CC the level of phenolic acids in plant cell walls of a transgenic plant by  
CC introducing into the plant an expression cassette comprising a promoter  
CC operably linked to a ferulic acid esterase encoding polynucleotide; and  
CC (2) a transgenic plant (II) produced by (M1). The transgenic plants are  
CC useful in improving digestibility for livestock and enhancing biomass  
CC conversion. The method is useful for enhancing the production of more  
CC highly fermentable carbohydrates in plants, especially forage grasses.  
CC The expression cassette is useful for controlling the level of phenolic  
CC acids in plant cell walls of a transgenic plant. The present sequence is  
CC used in the exemplification of the present invention.  
XX  
SQ Sequence 3657 BP; 916 A; 1012 C; 868 G; 860 T; 0 U; 1 Other;  
  
Query Match 15.1%; Score 236; DB 6; Length 3657;  
Best Local Similarity 100.0%; Pred. No. 1.9e-101;  
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1069 GAGCTCTCCCTCCCTCCCTCCGCGCGCGGTACACCCCGCTCTCTTC 1128  
Db GAGCTCTCTCCCTCCCTCCCTCCGCGCGCGGTACACCCCGCTCTCTTC 3369  
QY 1129 TTTCTCCGTTTTTTTTTGTGCTCGATCTTTGGCTTGTGATTTGGGTGGCG 1188  
Db TTTCTCCGTTTTTTTTTGTGCTCGATCTTTGGCTTGTGATTTGGGTGGCG 3429  
QY 1189 AGAGCGGCTTGTGCGCCAGATCGTGCGCGAGGCGGAGATCTCGCGCTGCGCTCT 1248  
Db 3430 AGAGCGGCTTGTGCGCCAGATCGTGCGCGAGGCGGAGATCTCGCGCTGCGCTCT 3489  
QY 1249 CCGGCGCTGAGTGCGCGCGGATCTCGCGGGAATGGGGCTCTCGAGTGTAGATCT 1304  
Db 3490 CCGGCGCTGAGTGCGCGCGGATCTCGCGGGAATGGGGCTCTCGAGTGTAGATCT 3545  
  
RESULT 14  
ADG69905  
ID ADG69905 standard; DNA; 4604 BP.  
XX  
AC ADG69905;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Vector pFQ10.1 nucleotide sequence.  
XX  
DE transgenic plant; ferulic acid esterase; FAE; enzyme; phenolic acid;  
KM plant; cell wall; improved digestibility; biomass conversion;  
KM highly fermentable carbohydrate; gene; ds.  
XX  
OS Synthetic.  
XX  
PN WO200268666-A1.  
XX  
PD 06-SEP-2002.  
XX  
PF 16-NOV-2001; 2001WO-US043588.  
XX  
PR 17-NOV-2000; 2000US-0249608P.

PA	(GENV ) GENENOCOR INT INC.
XX	
PI	Dunn-Coleman N, Langdon T, Morris P,
XX	
DR	WPI; 2002-696675/75.
XX	
PT	New transgenic plant comprising an expression cassette with a promoter
XX	
PR	operably linked to a fenilic acid esterase encoding polynucleotide,
PT	useful in improving digestibility for livestock and enhancing biomass
XX	
PS	conversion.
XX	
PS	Disclosure; Fig 45B-H; 208pp; English.
XX	
CC	The present invention describes a transgenic plant (1) comprising an
CC	expression cassette with a promoter operably linked to a fenilic acid
CC	esterase encoding polynucleotide. Also described: (1) controlling (M1)
CC	the level of phenolic acids in plant cell walls of a transgenic plant by
CC	introducing into the plant an expression cassette comprising a promoter
CC	operably linked to a fenilic acid esterase encoding polynucleotide; and
CC	(2) a transgenic plant (11) produced by (M1). The transgenic plants are
CC	useful in improving digestibility for livestock and enhancing biomass
CC	conversion. The method is useful for enhancing the production of more
CC	highly fermentable carbohydrates in plants, especially forage grasses.
CC	The expression cassette is useful for controlling the level of phenolic
CC	acids in plant cell walls of a transgenic plant. The present sequence is
CC	used in the exemplification of the present invention.
SQ	
	Sequence 4604 BP; 1161 A; 1222 C; 1117 G; 1104 T; 0 U; 0 Other;
	Query Match 15.1%; Score 236; DB 6; Length 4604;
	Beet Local Similarity 100.0%; Pred.No. 1.9e-101;
	Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	
	1069 GAGCTCCTCCCCCTTCCGCGCGCGCGGTAAACACCACCCTTCCTCTTTCC 1128
DB	4254 GAGCTCCTCCCCCTTCCGCGCGCGCGGTAAACACCACCCTTCCTCTTTCC 4313
OY	1129 TTTCCTGGTTTTTTTTTGTCGTCTGCATCTTTGSCCTTGGTAAGTTGGTGAGC 1168
DB	4314 TTTCCTCGTTTTTTTTTGTCGTCTGCATCTTTGSCCTTGGTAAGTTGGTGAGC 4373
OY	1189 AGAGGGGCTTCGTCCGCCCAAGATCGGTGGCGGGAAGGGCGGGATCTCCGCGCTGCGTCT 1248
DB	4374 AGAGGGGCTTCGTCCGCCCAAGATCGGTGGCGGGAAGGGCGGGATCTCCGCGCTGCGTCT 4433
OY	1249 CCGGGCGTAGAGTCGGGCGCGGATCTCTGGGAGGGAATTGGGACTCTGGGATGTGATCT 1304
DB	4434 CCGGGCGTAGAGTCGGGCGCGGATCTCTGGGAGGGAATTGGGACTCTGGGATGTGATCT 4489
	RESULT 15
	ADG69901
ID	ADG69901 standard; DNA; 4773 BP.
XX	
AC	ADG69901;
XX	
DT	11-MAR-2004 (first entry)
XX	
DE	Vector pGTS nucleotide sequence.
XX	
KM	transgenic plant; fenilic acid esterase; FAE; enzyme; phenolic acid;
KW	plant; cell wall; improved digestibility; biomass conversion;
KM	highly fermentable carbohydrate; gene; da.
XX	
OS	Synthetic.
PX	
PN	WO200268666-A1.
XX	
PD	06-SEP-2002.
XX	
PF	16-NOV-2001; 2001WO-USO43588.
XX	
PR	17-NOV-2000; 2000US--0249608P.

[illegible]

Search completed: September 12, 2005, 09:45:30  
Job time : 898.833 secs

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## OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 05:47:04 ; Search time 6651.44 Seconds  
(without alignments)  
8956.038 Million cell updates/sec

Title: US-10-758-799-3

Perfect score: 1565  
1 GAATTCCTGACAGTCACAGG.....TTTTTGTAGTAGACCAAG 1565

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	4.6	542	5 BQ609717	BQ609717 BRX_5803
2	55	3.5	293	8 CC001894	CC001894 PUBEC30TD
3	51	3.3	167	2 BE511568	BE511568 PUBEC6G11
4	51	3.3	349	6 CA617416	CA617416 wlin.pk00
5	51	3.3	453	6 CA624228	CA624228 wlin.pk01
6	51	3.3	457	6 CA623099	CA623099 wlin.pk01
7	51	3.3	522	6 CA626045	CA626045 wlin.pk01
8	51	3.3	551	7 CO532828	CO532828 3530.1.21
9	51	3.3	560	2 BE510680	BE510680 946054G04
10	51	3.3	585	6 CA832049	CA832049 111702780
11	51	3.3	643	6 CA620555	CA620555 wlin.pk00
12	51	3.3	660	6 BU572118	BU572118 946168B10
13	50	3.2	629	5 BU499258	BU499258 946173D07
14	47	2.9	840	8 BU499363	BU499363 946174D07
15	46	2.9	731	7 CO528948	CO528948 3530.1.19
16	43	2.7	572	8 B2541879	B2541879 OGABU04TM
17	43	2.7	605	5 BQ744771	BQ744771 946111B02
18	43	2.7	697	8 B2308389	B2308389 ic06e11.b
19	43	2.7	729	9 CC676920	CC676920 OGVESS0TV
20	43	2.7	731	8 B2324201	B2324201 ic06e11.9
21	43	2.7	840	9 CC340967	CC340967 OGRBK17TV
22	43	2.7	884	9 CG057952	CG057952 PUDK77TD
23	42	2.7	445	5 BQ744809	BQ744809 946111D08
24	42	2.7	520	8 CC044053	CC044053 3591.1_16

c	25	42	2.7	653	8 BH808262	BH808262 100807880
	26	42	2.7	795	6 CD437903	CD437903 EL01N0506
	27	42	2.7	825	9 CG117429	CG117429 PUTC12TB
	28	42	2.7	861	6 CD437683	CD437683 EL01N0503
	29	41	2.6	716	8 B2810022	B2810022 PUGER46TD
	30	40	2.6	863	9 CC734241	CC734241 OG0A018TH
	31	40	2.6	906	9 CC734247	CC734247 OG0A018TV
	32	39	2.5	790	8 B2985422	B2985422 PUG1227TD
	33	38	2.4	574	8 BH787841	BH787841 f2mb02010
	34	38	2.4	668	5 BU079606	BU079606 946145G02
	35	36	2.3	896	8 CC359562	CC359562 PUCB66TD
	36	36	2.3	954	8 CC359558	CC359558 PUCB66TD
	37	35	2.2	252	8 BH220473	BH220473 1006094G0
	38	35	2.2	254	8 B2755321	B2755321 PUGER87TB
	39	35	2.2	526	4 B1417123	B1417123 949053D12
	40	35	2.2	526	4 B1674155	B1674155 949053D12
	41	35	2.2	639	8 B2755322	B2755322 PUGER87TD
	42	35	2.2	771	8 B2751817	B2751817 PUDCT19TB
	43	35	2.2	771	8 B2751819	B2751819 PUDCT19TD
	44	35	2.2	785	8 B2987838	B2987838 PUDF850TD
	45	35	2.2	786	9 CG175670	CG175670 PUB1B35TD

## ALIGNMENTS

RESULT 1  
BQ609717 542 bp mRNA linear EST 25-JUN-2002  
LOCUS BRX\_5803 wheat EST endosperm library Triticum aestivum cDNA 5',  
DEFINITION mRNA sequence.  
ACCESSION BQ609717 GI:21559056  
VERSION BQ609717.1  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum

REFERENCE  
AUTHORS Clarke,B., Lambrecht,M. and Rhee,S.Y.  
TITLE Arabidopsis genomic information for interpreting wheat EST sequences  
JOURNAL Funct. Integr. Genomics 3 (1-2), 33-38 (2003)  
MEDLINE 22478026  
PUBMED 12590341

COMMENT  
Contact: Lambrecht M  
The Arabidopsis Information Resource  
Carnegie Institution of Washington, Dept. of Plant Biology  
260 Panama Street, Stanford, CA 94305, USA  
Tel: 1 650 325 1521 x 251  
Fax: 1 650 325 3748  
Email: rhee@acoma.stanford.edu.

## FEATURES

source  
1..542  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultivar="Wynna"  
/db\_xref="taxon:4565"  
/ribose\_type="endosperm"  
/dev\_stage="developing endosperm tissue 8, 10 and 12 DPA (days post anthesis)"  
/clone\_lib="wheat EST endosperm library"

## ORIGIN

Query Match 4.6% Score 72; DB 5; Length 542;  
Best Local Similarity 100.0%; Pred.No.4.1e-26;

Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1347 CGGCATGCTAAACACAGATCAGGAAGGAGGAAAGGCACTATGTTTATTTTATAT 1406  
DB 148 CGGCATGCTAAACACAGATCAGGAAGGAGGAAAGGCACTATGTTTATTTTATAT 207

QY 1407 ATTCTGCTGCT 1418  
 |||||  
 Db 208 ATTCTGCTGCT 219

RESULT 2  
 CC001894  
 LOCUS 293 bp DNA linear GSS 31-MAR-2003  
 DEFINITION PUB03J07D\_ZM\_0\_6\_1\_0\_KB Zea mays genomic clone ZMBR196E11,  
 genomic survey sequence.  
 CC001894  
 ACCESSION CC001894  
 VERSION CC001894.1 GI:29380454  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 293)  
 Whitefaw,C.A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
 Benmetzen,U.  
 Maize Genomics Consortium  
 Unpublished (2003)  
 COMMENT Contact: Cathy Whitelaw  
 TIGR  
 912 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whitefaw@tigr.org  
 Seq primer: TP  
 Class: sheared ends.

FEATURES  
 source  
 1..293  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone\_lib="ZM\_0\_6\_1\_0\_KB"  
 /note="Vector: pCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 Cor selected genomic DNA library"

ORIGIN  
 Query Match 3.5%; Score 55; DB 8; Length 293;  
 Best Local Similarity 100.0%; Pred.No. 4,2e-17;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 819 ACCGCGATCGCTCCCTACGCTTCCACCTCATCGGCGCGCTCCATCTCCATCCACA 873  
 |||||  
 Db 208 ACCGCGATCGCTCCCTACGCTTCCACCTCATCGGCGCGCTCCATCTCCATCCACA 262

RESULT 3  
 BS511568  
 LOCUS 167 bp mRNA linear EST 07-AUG-2000  
 DEFINITION 946061G11.y1 946 - tassels primordium prepared by Schmidt lab Zea  
 mays cDNA, mRNA sequence.  
 BS511568  
 ACCESSION BS511568  
 VERSION BS511568.1 GI:9732816  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 167)  
 Walbot,V  
 Maize ESTs from various cDNA libraries sequenced at Stanford  
 University  
 Unpublished (1999)  
 COMMENT Contact: Walbot V  
 Department of Biological Sciences

Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 946061 row: G column: 11.  
 Location/Qualifiers  
 1..167  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="OH43"  
 /db\_xref="taxon:4577"  
 /tissue\_type="tassels"  
 /dev\_stage="just after the transition from vegetative to  
 inflorescence development"  
 /lab\_host="Y10LR"  
 /clone\_lib="946 - tassels primordium prepared by Schmidt  
 lab"  
 /note="Organ: tassels; Vector: HybridZAP; Site\_1: EcoRI;  
 Site\_2: XhoI; George Chuck dissected immature tassels  
 between 1mm and 3mm. Sharon Stanfield prepared the cDNA  
 library in HybridZAP. Sample insert size range was 350 bp  
 to 3 Kb with a 1 Kb average."

ORIGIN  
 Query Match 3.3%; Score 51; DB 2; Length 167;  
 Best Local Similarity 100.0%; Pred.No. 5,6e-15;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 997 CCCAATTCGACGCTGCGACCAACTGCGCTCTCCGCGGCAAGCAACAAAG 1047  
 |||||  
 Db 2 CCCAATTCGACGCTGCGACCAACTGCGCTCTCCGCGGCAAGCAACAAAG 52

RESULT 4  
 CA617416  
 LOCUS 349 bp mRNA linear EST 23-NOV-2002  
 DEFINITION w1ln.pk0018.c3 w1ln Triticum aestivum cDNA clone w1ln.pk0018.c3 5'  
 end, mRNA sequence.  
 CA617416  
 ACCESSION CA617416.1 GI:25195713  
 VERSION  
 KEYWORDS EST.  
 SOURCE Triticum aestivum (bread wheat)  
 ORGANISM Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Pooidaeae; Triticeae; Triticum.  
 1 (bases 1 to 349)  
 Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,  
 Miao,G., Caraher,N. and Hanafey,M.K.  
 Dupont Wheat cDNA Sequence  
 Unpublished (2002)  
 COMMENT Contact: Scott V. Tingey  
 Crop Genetics  
 E. I. Dupont de Nemours and Company  
 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA  
 Tel: 302-631-2602  
 Fax: 302-631-2607  
 Email: Scott.V.Tingey@usa.dupont.com  
 Seq primer: M13.  
 Location/Qualifiers  
 1..349  
 /organism="Triticum aestivum"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4565"  
 /clone="w1ln.pk0018.c3"  
 /tissue\_type="leaf"  
 /clone\_lib="w1ln"  
 /note="Vector: pBluescript SK+, Site\_1: EcoRI, Site\_2:  
 XhoI; wheat (Triticum aestivum L.) leaf 7 day old  
 seedling, light grown (normalized)";

ORIGIN

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Query Match          3.3%; Score 51; DB 6; Length 349;
Best Local Similarity 100.0%; Pred. No. 5.5e-15;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 997 CCCAATTCCAGCGTGCACCACTCGCGCTCTCCGCGCCAGACCAAG 1047
|||||
17 CCCAATTCCAGCGTGCACCACTCGCGCTCTCCGCGCCAGACCAAG 67

RESULT 5
CA624228          453 bp  mRNA  linear  EST 23-NOV-2002
LOCUS             wlin.pk0138.e1 wlin Triticum aestivum cDNA clone wlin.pk0138.e1 5'
DEFINITION        end, mRNA sequence.
ACCESSION         CA624228
VERSION           CA624228.1 GI:25202524
KEYWORDS
SOURCE
ORGANISM          Triticum aestivum (bread wheat)
                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                  Poideae; Triticeae; Triticum.
                  1 (bases 1 to 453)
REFERENCE
AUTHORS           Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
                  Miao,G., Caraher,N. and Hanafey,M.K.
TITLE             Dupont Wheat cDNA Sequence
JOURNAL           Unpublished (2002)
COMMENT           Contact: Scott V. Tingey
                  Crop Genetics
                  E.I. Dupont de Nemours and Company
                  1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
                  Tel: 302-631-2607
                  Fax: 302-631-2607
                  Email: Scott.V.Tingey@USA.dupont.com
                  Seq primer: M13.
FEATURES
Source            Location/Qualifiers
                  1..453
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                  /mol_type="mRNA"
                  /db_xref="taxon:4565"
                  /clone="wlin.pk0138.e1"
                  /issue_type="leaf"
                  /clone_lib="wlin"
                  /note="Vector: pBluescript SK+, Site 1: EcoRI, Site 2:
                  XhoI; wheat (Triticum aestivum L.) leaf 7 day old
                  seedling, light grown (normalized)"

ORIGIN
Query Match          3.3%; Score 51; DB 6; Length 453;
Best Local Similarity 100.0%; Pred. No. 5.5e-15;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 997 CCCAATTCCAGCGTGCACCACTCGCGCTCTCCGCGCCAGACCAAG 1047
|||||
10 CCCAATTCCAGCGTGCACCACTCGCGCTCTCCGCGCCAGACCAAG 60

RESULT 6
CA623099          457 bp  mRNA  linear  EST 23-NOV-2002
LOCUS             wlin.pk0090.d12 wlin Triticum aestivum cDNA clone wlin.pk0090.d12
DEFINITION        5' end, mRNA sequence.
ACCESSION         CA623099
VERSION           CA623099.1 GI:25201395
KEYWORDS
SOURCE
ORGANISM          Triticum aestivum (bread wheat)
                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                  Poideae; Triticeae; Triticum.
                  1 (bases 1 to 457)
REFERENCE
AUTHORS           Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
                  Miao,G., Caraher,N. and Hanafey,M.K.

ORIGIN
Query Match          3.3%; Score 51; DB 6; Length 457;
Best Local Similarity 100.0%; Pred. No. 5.5e-15;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 997 CCCAATTCCAGCGTGCACCACTCGCGCTCTCCGCGCCAGACCAAG 1047
|||||
12 CCCAATTCCAGCGTGCACCACTCGCGCTCTCCGCGCCAGACCAAG 62

RESULT 7
CA626045          522 bp  mRNA  linear  EST 23-NOV-2002
LOCUS             wlin.pk0138.b11 wlin Triticum aestivum cDNA clone wlin.pk0138.b11
DEFINITION        5' end, mRNA sequence.
ACCESSION         CA626045
VERSION           CA626045.1 GI:25204341
KEYWORDS
SOURCE
ORGANISM          Triticum aestivum (bread wheat)
                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                  Poideae; Triticeae; Triticum.
                  1 (bases 1 to 522)
REFERENCE
AUTHORS           Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
                  Miao,G., Caraher,N. and Hanafey,M.K.
TITLE             Dupont Wheat cDNA Sequence
JOURNAL           Unpublished (2002)
COMMENT           Contact: Scott V. Tingey
                  Crop Genetics
                  E.I. Dupont de Nemours and Company
                  1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
                  Tel: 302-631-2602
                  Fax: 302-631-2607
                  Email: Scott.V.Tingey@USA.dupont.com
                  Seq primer: M13.
FEATURES
Source            Location/Qualifiers
                  1..522
                  /organism="Triticum aestivum"
                  /mol_type="mRNA"
                  /db_xref="taxon:4565"
                  /clone="wlin.pk0138.b11"
                  /issue_type="leaf"
                  /clone_lib="wlin"
                  /note="Vector: pBluescript SK+, Site 1: EcoRI, Site 2:
                  XhoI; wheat (Triticum aestivum L.) leaf 7 day old
                  seedling, light grown (normalized)"

ORIGIN
Query Match          3.3%; Score 51; DB 6; Length 522;
Best Local Similarity 100.0%; Pred. No. 5.5e-15;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 997 CCCAATTCCAGCGTGCACCACTCGCGCTCTCCGCGCCAGACCAAG 1047
|||||
12 CCCAATTCCAGCGTGCACCACTCGCGCTCTCCGCGCCAGACCAAG 62

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Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 997 CCCAATTCAGCGCTGCCACCAACTGCGCGTCTCCGCGCAAGCAACCAAG 1047

Db 12 CCCAATTCAGCGCTGCCACCAACTGCGCGTCTCCGCGCAAGCAACCAAG 62

RESULT 8  
COS32828 551 bp mRNA 1linear EST 15-JUL-2004  
LOCUS 3530\_1.216.1.A05.V.1.3530 - Full length cDNA library created by  
DEFINITION Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.

ACCESSION COS32828  
VERSION COS32828.1 GI:50337702  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 551)  
Malbot.V.

AUTHORS Maize ESTs from various cDNA libraries sequenced at Stanford

TITLE University

JOURNAL Unpublished (1999)

COMMENT Contact: Malbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 3530.1.216.1 row: A column: 05.

Location/Qualifiers

1..551

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="B73"

/db\_xref="taxon:4577"

/tissue\_type="multiple"

/dev\_stage="varies by tissue"

/lab\_host="PH108"

/clone\_lib="3530 - Full length cDNA library created by

Invitrogen from multiple tissues"

/note="Organ: silks, husks, ears, pollen, shoot tips,

leaf, root tips, whole seed, embryo; Vector: pCMV-SORT

6.1; Site\_1: EcoRV; Site\_2: NotI; Maize Gene Discovery

Project contracted with Invitrogen to produce a

normalized, full length library in a pSport vector. This

is a Gateway compatible vector, permitting clone movement

to new vector backbones for expression in diverse host

cells using recombination rather than restriction enzymes.

Details of the vector and sequencing primers are available

at ZmDB in the EST library description tables. poly(A)+

mRNA was prepared by Invitrogen, and equimolar amounts of

RNA from each of the 12 tissue samples were mixed together

for selection of mRNA with a 5' cap. After synthesis of

cDNA, a normalization step was conducted against the

mixture of RNA sources. This step effected a 20X to 80X

reduction in common transcript types. Tissues prepared: 1.

just emerging silks; 2. inner husks from ears of sample

#1; 3. 20 day aleurone; 4. immature tassels, stages from

1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm

vegetative shoot tips from 15 day old seedlings; all

leaves with an expanded or partially expanded sheath

were removed; 8. mature leaf tissue; 9. 0.5 cm long root

tips from 15 day old seedlings; 10. 10 day whole seed; 11.

12 day endosperm and embryo; 12. 17 day endosperm and

embryo. All of the sequenced clones in project 3530 will

be archived at the University of Arizona along with the

UniGene clones from the Maize Gene Discovery EST

sequencing projects. Clones can be ordered through the

ZmDB web site or directly from the University of Arizona

(http://www.genome.arizona.edu/orders/). High density  
filters containing over 18,000 clones can also be ordered  
from the University of Arizona."

Query Match 3.3%; Score 51; DB 7; Length 551;  
Best Local Similarity 100.0%; Pred. No. 5.5e-15;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 997 CCCAATTCAGCGCTGCCACCAACTGCGCGTCTCCGCGCAAGCAACCAAG 1047

Db 18 CCCAATTCAGCGCTGCCACCAACTGCGCGTCTCCGCGCAAGCAACCAAG 68

RESULT 9

BE510680

560 bp mRNA 1linear EST 07-AUG-2000

LOCUS 946054G04.y1.946 - tassel primordium prepared by Schmidt lab Zea

DEFINITION mays cDNA, mRNA sequence.

ACCESSION BE510680

VERSION BE510680.1 GI:9731928

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 560)

Malbot.V.

AUTHORS Maize ESTs from various cDNA libraries sequenced at Stanford

TITLE University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 946054 row: G column: 04.

Location/Qualifiers

1..560

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="OH43"

/db\_xref="taxon:4577"

/tissue\_type="tassel"

/dev\_stage="just after the transition from vegetative to

inflorescence development"

/lab\_host="XLOLR"

/clone\_lib="946 - tassel primordium prepared by Schmidt

lab"

/note="Organ: tassels; Vector: HybridZAP; Site\_1: EcoRI;

Site\_2: XhoI; George Chuck dissected immature tassels

between 1mm and 3mm. Sharon Stanfield prepared the cDNA

library in HybridZAP. Sample insert size range was 350 bp

to 3 Kb with a 1 Kb average."

ORIGIN

Query Match 3.3%; Score 51; DB 2; Length 560;  
Best Local Similarity 100.0%; Pred. No. 5.4e-15;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 997 CCCAATTCAGCGCTGCCACCAACTGCGCGTCTCCGCGCAAGCAACCAAG 1047

Db 2 CCCAATTCAGCGCTGCCACCAACTGCGCGTCTCCGCGCAAGCAACCAAG 52

RESULT 10

CAB32049

585 bp mRNA 1linear EST 12-DEC-2002

LOCUS 1117027B07.y1.1117 - UniGene V from Maize Genome Project Zea mays

DEFINITION cDNA, mRNA sequence.

ACCESSION CA832049  
 VERSION CA832049.1 GI:26559814  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Bkaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 585)  
 Maibot, V.  
 Zea ESTs from various cDNA libraries sequenced at Stanford  
 University  
 TITLE  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Walbot, V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 117027 row: B column: 07.  
 Location/Qualifiers  
 1..585  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4577"  
 /clone\_id="1117 - Unigene V from Maize Genome Project"  
 /note="This library represents the unique genes found in  
 the fifth round of EST sequencing at Stanford University  
 for the maize genome project. Sequences are present from  
 library 946. Contigs were assembled using ZmDBAssembler  
 and 2 representatives from each contig were selected for  
 the Unigene set. All singlets were also selected."

ORIGIN  
 Query Match 3.3%; Score 51; DB 6; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-15;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 997 CCCAATTCACGCTGCACCACTCCGCTCTCCGCGCCAGCAACCAAG 1047  
 |||||  
 13 CCCAATTCACGCTGCACCACTCCGCTCTCCGCGCCAGCAACCAAG 63

RESULT 11  
 CA620555 643 bp mRNA linear EST 23-NOV-2002  
 LOCUS w1ln.pk0056.d1 w1ln Triticum aestivum cDNA clone w1ln.pk0056.d1 5'  
 DEFINITION end, mRNA sequence.  
 ACCESSION CA620555  
 VERSION CA620555.1 GI:25198851  
 KEYWORDS EST.  
 SOURCE Triticum aestivum (bread wheat)  
 ORGANISM Triticum aestivum  
 Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Triticum.  
 1 (bases 1 to 643)  
 Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,  
 Miao, G., Caraher, N. and Hanafey, M.K.  
 Dupont Wheat cDNA Sequence  
 Unpublished (2002)  
 Contact: Scott V. Tingey  
 Crop Genetics  
 E. I. Dupont de Nemours and Company  
 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA  
 Tel: 302-631-2602  
 Fax: 302-631-2607  
 Email: Scott.V.Tingey@USA.dupont.com  
 Seq primer: ML3.  
 Location/Qualifiers  
 1..643  
 /organism="Triticum aestivum"

FEATURES  
 source

ORIGIN  
 Query Match 3.3%; Score 51; DB 6; Length 643;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-15;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 997 CCCAATTCACGCTGCACCACTCCGCTCTCCGCGCCAGCAACCAAG 1047  
 |||||  
 18 CCCAATTCACGCTGCACCACTCCGCTCTCCGCGCCAGCAACCAAG 68

RESULT 12  
 BU572118 660 bp mRNA linear EST 16-SEP-2002  
 LOCUS 946168B10.y1 946 - tassal primordium prepared by Schmidt lab Zea  
 DEFINITION mays cDNA, mRNA sequence.  
 ACCESSION BU572118 GI:22935843  
 VERSION BU572118.1  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Bkaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 660)  
 Maibot, V.  
 Zea ESTs from various cDNA libraries sequenced at Stanford  
 University  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Walbot, V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 946168 row: B column: 10.  
 Location/Qualifiers  
 1..660  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:4577"  
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 /dev\_stage="just after the transition from vegetative to  
 inflorescence development"  
 /lab\_note="XLOLR"  
 /clone\_id="946 - tassal primordium prepared by Schmidt  
 lab"  
 /note="Organ: tassels; Vector: HybridZAP; Site 1: EcoRI;  
 Site 2: XhoI; George Chuck dissected immature tassels  
 between 1mm and 3mm. Sharon Stanfield prepared the cDNA  
 library in HybridZAP. Sample insert size range was 350 bp  
 to 3 Kb with a 1 Kb average."

ORIGIN  
 Query Match 3.3%; Score 51; DB 5; Length 660;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-15;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 997 CCCAATTCACGCTGCACCACTCCGCTCTCCGCGCCAGCAACCAAG 1047  
 |||||  
 15 CCCAATTCACGCTGCACCACTCCGCTCTCCGCGCCAGCAACCAAG 65

FEATURES  
 source

RESULT 13  
 BUA99258 629 bp mRNA linear EST 12-SEP-2002  
 LOCUS 946173D07.y1 946 - tassels primordium prepared by Schmidt lab Zea  
 DEFINITION  
 ACCESSION BUA99258  
 VERSION BUA99258.1 GI:22819168  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.  
 1 (bases 1 to 629)  
 Walbot,V.  
 Maize ESTs from various cDNA libraries sequenced at Stanford University  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 946173 row: D column: 07.

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 /clone\_1lb="946 - tassels primordium prepared by Schmidt lab"  
 /note="Organ: tassels; Vector: HybridZAP; Site 1: EcoRI; Site 2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybridZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."

ORIGIN  
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 Best Local Similarity 100.0%; Pred. No. 1.8e-14;  
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 LOCUS 946174D07.y1 946 - tassels primordium prepared by Schmidt lab Zea  
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 VERSION BUA99363.1 GI:22819273  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.  
 1 (bases 1 to 586)  
 Walbot,V.  
 Maize ESTs from various cDNA libraries sequenced at Stanford University  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Walbot V

Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 946174 row: D column: 07.

FEATURES  
 source  
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 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="OH43"  
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 /tissue\_type="tassels"  
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 /clone\_1lb="946 - tassels primordium prepared by Schmidt lab"  
 /note="Organ: tassels; Vector: HybridZAP; Site 1: EcoRI; Site 2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybridZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."

ORIGIN  
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 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 VERSION COS28948.1 GI:50333822  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
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 1 (bases 1 to 731)  
 Walbot,V.  
 Maize ESTs from various cDNA libraries sequenced at Stanford University  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 3530\_1.191.1 row: B column: 09.

FEATURES  
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 /note="Organ: silks, husks, ears, pollen, shoot tips,"



leaf, root tips, whole seed, embryo; Vector: PCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Gene Discovery Project contracted with Invitrogen to produce a normalized, full length library in a pSport vector. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. Details of the vector and sequencing primers are available at ZmDB in the EST library description tables. poly(A) + mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. This step effected a 20X to 80X reduction in common transcript types. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in project 3530 will be archived at the University of Arizona along with the UniGene clones from the Maize Gene Discovery EST sequencing projects. Clones can be ordered through the ZmDB web site or directly from the University of Arizona (<http://www.genome.arizona.edu/orders/>). High density filters containing over 10,000 clones can also be ordered from the University of Arizona."

## ORIGIN

Query Match 2.9%; Score 46; DB 7; Length 731;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-12;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 34 TTCCACGCTGCGACCAACTGCGCTCTCCGCGCCAGACACCAAG 79

Search completed: September 12, 2005, 14:04:13  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 08:43:13 ; Search time 435.627 Seconds  
(without alignments)  
5878.368 Million cell updates/sec

Title: US-10-758-799-3

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Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	1021	65.2	1021	US-09-037-531-1	Sequence 1, Appl1
3	454	29.0	454	US-09-037-531-2	Sequence 2, Appl1
4	296	18.9	623	US-09-078-862-5	Sequence 5, Appl1
5	296	18.9	1392	US-08-144-602B-6	Sequence 6, Appl1
6	296	18.9	1404	US-08-144-602B-7	Sequence 7, Appl1
7	296	18.9	2199	US-08-144-602B-5	Sequence 5, Appl1
8	296	18.9	5643	US-08-144-602B-4	Sequence 4, Appl1
9	145	9.3	4032	US-09-068-101-5	Sequence 5, Appl1
10	145	9.3	4032	US-09-970-921-5	Sequence 5, Appl1
11	140	8.9	3039	US-09-377-466B-19	Sequence 19, Appl1
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13	140	8.9	3044	US-09-377-466B-38	Sequence 18, Appl1
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44	23	1.5	92	US-08-912-951-327	Sequence 327, App
45	23	1.5	92	US-09-402-181B-614	Sequence 614, App

#### ALIGNMENTS

##### RESULT 1

US-09-037-531-3  
Sequence 3, Application US/09037531

Patent No. 6750378

GENERAL INFORMATION:

APPLICANT: Derose, Richard

TITLE OF INVENTION: Maize H3C4 Promoter Combined With The

TITLE OF INVENTION: First Intron Of Rice Actin, Chimeric Gene Comprising It

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESSES:

ADDRESSER: Connolly, Bove, Lodge, & Hutz

STREET: 1220 Market Street

CITY: Wilmington

STATE: DE

COUNTRY: USA

ZIP: 19899

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/037, 531

FILING DATE: 10-MAR-1998

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: McMorrow Jr., Robert G.

REGISTRATION NUMBER: 30962

REFERENCE/DOCKET NUMBER: 5500\*24

TELECOMMUNICATION INFORMATION:

TELEPHONE: (302)658-9141

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1565 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-037-531-3

Query Match 100.0% Score 1565; DB 4; Length 1565;  
Best local Similarity 100.0%; Pred. No. 0;

Matches 1565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 2

US-09-037-531-1

Sequence 1, Application US/09037531

Patent No. 6750378

GENERAL INFORMATION:

APPLICANT: DeRose, Richard

TITLE OF INVENTION: Maize H3C4 Promoter Combined With The

TITLE OF INVENTION: First Intron Of Rice Actin, Chimeric Gene Comprising It

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESS: Connolly, Bove, Lodge, &amp; Hutz

STREET: 1220 Market Street

CITY: Wilmington

STATE: DE

COUNTRY: USA

ZIP: 19899

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/037,531

FILING DATE: 10-MAR-1998

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: McMorrow Jr., Robert G.

REGISTRATION NUMBER: 30962

REFERENCE/DOCKET NUMBER: 5500\*24

TELECOMMUNICATION INFORMATION:

TELEPHONE: (302) 658-9141

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1021 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-037-531-1

Query Match 65.2%; Score 1021; DB 4; Length 1021;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1021; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3  
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 ; Patent No. 6750378  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Derose, Richard  
 ; TITLE OF INVENTION: Freysinet, Georges  
 ; TITLE OF INVENTION: Maize H3C4 Promoter Combined With The  
 ; TITLE OF INVENTION: First Intron Of Rice Actin, Chimeric Gene Comprising It  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Connolly, Bove, Lodge, & Hutz  
 ; STREET: 1220 Market Street  
 ; CITY: Wilmington  
 ; STATE: DE  
 ; COUNTRY: USA  
 ; ZIP: 19899  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/037,531  
 ; FILING DATE: 10-MAR-1998  
 ; CLASSIFICATION: 800  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: McMorrow Jr., Robert G.  
 ; REGISTRATION NUMBER: 30962  
 ; REFERENCE/DOCKET NUMBER: 5500\*24  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (302)658-9141  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 454 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; US-09-037-531-2

Query Match 29.0%; Score 454; DB 4; Length 454;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-211; Indels 0; Gaps 0;  
 Matches 454; Conservative 0; Mismatches 0;

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QY 1102 GTACACACCCGCCCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTGAT 1161
DB 1 GTACACACCCGCCCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTGAT 60
QY 1162 CTTTGGCTTTGATGTTGGGTGGGAGAGCGGCTTCTCGCCAGATCGGCGGG 1221
DB 61 CTTTGGCTTTGATGTTGGGTGGGAGAGCGGCTTCTCGCCAGATCGGCGGG 120
QY 1222 AGGGGGGAGATCTCGGGGCTGCGCTCCGGGCGTGAAGTCCGCCGAGATCTCGCGGGGA 1281
DB 121 AGGGGGGAGATCTCGGGGCTGCGCTCCGGGCGTGAAGTCCGCCGAGATCTCGCGGGGA 180
QY 1282 ATGGGGCTCTCGGATGTAGATCGGCGGTTGTTGGGGAGATGATGAGGGCGTTTAA 1341
DB 181 ATGGGGCTCTCGGATGTAGATCGGCGGTTGTTGGGGAGATGATGAGGGCGTTTAA 240
QY 1342 AATTTGCCATGTCTAAAGATCAGGAGAGAGGGGAAAAAGGCACTATGTTATTTT 1401
DB 241 AATTTGCCATGTCTAAAGATCAGGAGAGAGGGGAAAAAGGCACTATGTTATTTT 300
QY 1402 TATATATTTCTGCTGCTCGTCAAGGCTTAGATGATGATCTTCTTCTTCTTCTT 1461

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Db 301 TATATATTTCTGCTGCTGCTGCTGACGAGCTAGATGATGCTTTCTTTCTTTT 360  
QY 1462 GGGGGAGAAATTTGATCCCTCGATGATGTTGATCGGTGTTTCTTTTCAAGATTGT 1521  
Db 361 GGGGGAGAAATTTGAAATCCCTCGACATGTTGATCGGTGTTTCTTTTCAAGATTGT 420  
QY 1522 GACAAATGACGCTCGTGGCGAGACTTTTGTAG 1555  
Db 421 GACAAATGACGCTCGTGGCGAGACTTTTGTAG 454

## RESULT 4

US-09-078-862-5  
; Sequence 5, Application US/09078862  
; Patent No. 6091003  
; GENERAL INFORMATION:  
; APPLICANT: Nan, Guo-Ling  
; APPLICANT: Nagai, Chifumi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENETIC  
; TITLE OF INVENTION: TRANSFORMATION OF PINEAPPLE  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Medlen & Carroll, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/078,862  
; FILING DATE: 14-MAY-1998  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Carroll, Peter G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: UH-03321  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 623 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
US-09-078-862-5

Query Match 18.9%; Score 296; DB 3; Length 623;

Best Local Similarity 100.0%; Pred. No. 2,2e-134; Indels 0; Gaps 0;

Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1265 CCGGATCTTCGCGGGGAATGGGCTCTCGGATGTAGATCTGATCCGCGTGTGGGGGA 1324  
Db 278 CCGGATCTTCGCGGGGAATGGGCTCTCGGATGTAGATCTGATCCGCGTGTGGGGGA 337  
QY 1325 GAGGATGGGCGCTTTAAATTTGGCCATGCTAAACAAGATCAGAAAGAGGGAAGGCG 1384  
Db 338 GAGGATGGGCGCTTTAAATTTGGCCATGCTAAACAAGATCAGAAAGAGGGAAGGCG 397  
QY 1385 ACTATGGTTAATTTTATATATTTCTGCTGCTGCTGCTAGAGCTTAGATGTAGAT 1444  
Db 398 ACTATGGTTAATTTTATATATTTCTGCTGCTGCTGCTAGAGCTTAGATGTAGAT 457  
QY 1445 CTTTCTTTCTTTCTTTTGTGGGTAGAAATTTGAATCCCTCGACATGTTTCATCGGTAGTT 1504  
Db 458 CTTTCTTTCTTTCTTTTGTGGGTAGAAATTTGAATCCCTCGACATGTTTCATCGGTAGTT 517

QY 1505 TTCTTTTCATGATTTGTGACAAATGACAGCTGTCGGAGCTTTTGTAGGTAGA 1560  
Db 518 TTCTTTTCATGATTTGTGACAAATGACAGCTGTCGGAGCTTTTGTAGGTAGA 573

## RESULT 5

US-08-144-602B-6  
; Sequence 6, Application US/08144602B  
; Patent No. 5641876  
; GENERAL INFORMATION:  
; APPLICANT: McElroy, David  
; APPLICANT: Wu, Ray  
; TITLE OF INVENTION: RICE ACTIN GENE AND PROMOTER  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP  
; STREET: CLINTON SQUARE, P.O. BOX 1051  
; CITY: ROCHESTER  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 14603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/144,602B  
; FILING DATE: 27-OCT-1993  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: TIMIAN, SUSAN J.  
; REGISTRATION NUMBER: 34,103  
; REFERENCE/DOCKET NUMBER: 19603/10140  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 716-263-1636  
; TELEFAX: 716-263-1600  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1392 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-144-602B-6

Query Match 18.9%; Score 296; DB 1; Length 1392;

Best Local Similarity 100.0%; Pred. No. 2,2e-134; Indels 0; Gaps 0;

Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1265 CCGGATCTTCGCGGGGAATGGGCTCTCGGATGTAGATCTGATCCGCGTGTGGGGGA 1324  
Db 1076 CCGGATCTTCGCGGGGAATGGGCTCTCGGATGTAGATCTGATCCGCGTGTGGGGGA 1135  
QY 1325 GAGGATGGGCGCTTTAAATTTGGCCATGCTAAACAAGATCAGAAAGAGGGAAGGCG 1384  
Db 1136 GAGGATGGGCGCTTTAAATTTGGCCATGCTAAACAAGATCAGAAAGAGGGAAGGCG 1195  
QY 1385 ACTATGGTTAATTTTATATATTTCTGCTGCTGCTGCTAGAGCTTAGATGTAGAT 1444  
Db 1196 ACTATGGTTAATTTTATATATTTCTGCTGCTGCTGCTAGAGCTTAGATGTAGAT 1255  
QY 1445 CTTTCTTTCTTTCTTTTGTGGGTAGAAATTTGAATCCCTCGACATGTTTCATCGGTAGTT 1504  
Db 1256 CTTTCTTTCTTTCTTTTGTGGGTAGAAATTTGAATCCCTCGACATGTTTCATCGGTAGTT 1315  
QY 1505 TTCTTTTCATGATTTGTGACAAATGACAGCTGTCGGAGCTTTTGTAGGTAGA 1560  
Db 1316 TTCTTTTCATGATTTGTGACAAATGACAGCTGTCGGAGCTTTTGTAGGTAGA 1371

## RESULT 6

```
US-08-144-602B-7
; Sequence 7, Application US/08144602B
; Patent No. 5641876
; GENERAL INFORMATION:
; APPLICANT: McElroy, David
; APPLICANT: Wu, Ray
; TITLE OF INVENTION: RICE ACTIN GENE AND PROMOTER
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
; STREET: CLINTON SQUARE, P.O. BOX 1051
; CITY: ROCHESTER
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/144,602B
; FILING DATE: 27-OCT-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: TIMIAN, SUSAN J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 19603/10140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1636
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
;
US-08-144-602B-7
Query Match 18.9%; Score 296; DB 1; Length 1404;
Best Local Similarity 100.0%; Pred. No. 2.2e-134;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1265 CCGGATCTCGCGGGGAATGCGGCTCTCGGATGTAGATCGGCGGTTGTGGGGGA 1324
DB 1086 CCGGATCTCGCGGGGAATGCGGCTCTCGGATGTAGATCGGCGGTTGTGGGGGA 1145
QY 1325 GATGATGGGCGGTTAAATTTCCGATGCTAAACAAGATCAGAGAGAGGGGAAAAGGCG 1384
DB 1146 GATGATGGGCGGTTAAATTTCCGATGCTAAACAAGATCAGAGAGAGGGGAAAAGGCG 1205
QY 1385 ACTATGTTTATATTTTATATATTTCTGCTGCTGCTGCTGCTAGATGCTAGAT 1444
DB 1206 ACTATGTTTATATTTTATATATTTCTGCTGCTGCTGCTGCTAGATGCTAGAT 1265
QY 1445 CTTCCTTTCTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCAATGTTCAATCGGTAGTT 1504
DB 1266 CTTCCTTTCTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCAATGTTCAATCGGTAGTT 1325
QY 1505 TTCTTTTCATGATTTGTGACAAATGACGCTCGTGGGAGCTTTTGTGAGTGA 1560
DB 1326 TTCTTTTCATGATTTGTGACAAATGACGCTCGTGGGAGCTTTTGTGAGTGA 1381
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RESULT 7  
US-08-144-602B-5  
; Sequence 5, Application US/08144602B  
; Patent No. 5641876  
; GENERAL INFORMATION:  
; APPLICANT: McElroy, David  
; APPLICANT: Wu, Ray  
; TITLE OF INVENTION: RICE ACTIN GENE AND PROMOTER

```
NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
; STREET: CLINTON SQUARE, P.O. BOX 1051
; CITY: ROCHESTER
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/144,602B
; FILING DATE: 27-OCT-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: TIMIAN, SUSAN J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 19603/10140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1636
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2199 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
;
US-08-144-602B-5
Query Match 18.9%; Score 296; DB 1; Length 2199;
Best Local Similarity 100.0%; Pred. No. 2.2e-134;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1265 CCGGATCTCGCGGGGAATGCGGCTCTCGGATGTAGATCGGCGGTTGTGGGGGA 1324
DB 1883 CCGGATCTCGCGGGGAATGCGGCTCTCGGATGTAGATCGGCGGTTGTGGGGGA 1942
QY 1325 GATGATGGGCGGTTAAATTTCCGATGCTAAACAAGATCAGAGAGAGGGGAAAAGGCG 1384
DB 1943 GATGATGGGCGGTTAAATTTCCGATGCTAAACAAGATCAGAGAGAGGGGAAAAGGCG 2002
QY 1385 ACTATGTTTATATTTTATATATTTCTGCTGCTGCTGCTGCTAGATGCTAGAT 1444
DB 2003 ACTATGTTTATATTTTATATATTTCTGCTGCTGCTGCTGCTAGATGCTAGAT 2062
QY 1445 CTTCCTTTCTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCAATGTTCAATCGGTAGTT 1504
DB 2063 CTTCCTTTCTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCAATGTTCAATCGGTAGTT 2122
QY 1505 TTCTTTTCATGATTTGTGACAAATGACGCTCGTGGGAGCTTTTGTGAGTGA 1560
DB 2123 TTCTTTTCATGATTTGTGACAAATGACGCTCGTGGGAGCTTTTGTGAGTGA 2178
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RESULT 8  
US-08-144-602B-4  
; Sequence 4, Application US/08144602B  
; Patent No. 5641876  
; GENERAL INFORMATION:  
; APPLICANT: McElroy, David  
; APPLICANT: Wu, Ray  
; TITLE OF INVENTION: RICE ACTIN GENE AND PROMOTER  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP  
; STREET: CLINTON SQUARE, P.O. BOX 1051  
; CITY: ROCHESTER  
; STATE: NEW YORK  
; COUNTRY: USA

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; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/144,602B
; FILING DATE: 27-OCT-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: TIMIAN, SUSAN J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 19603/10140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1636
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5643 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-144-602B-4

Query Match      18.9%; Score 296; DB 1; Length 5643;
Best Local Similarity 100.0%; Pred. No. 2.2e-134;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1265 CCGGATCTCCGCGGGAATGGGCTCTCGATGTAGATCCGCCGTTGTGGGGG 1324
DB      1886 CCGGATCTCCGCGGGAATGGGCTCTCGATGTAGATCCGCCGTTGTGGGGG 1945
QY      1325 GATGATGGGGCGTTTAAATTTGCGCATGCTAAACAAGATCAGAGAGGGGAAAAGGCG 1384
DB      1946 GATGATGGGGCGTTTAAATTTGCGCATGCTAAACAAGATCAGAGAGGGGAAAAGGCG 2005
QY      1385 ACTATGGTTATATTTTATATATTTCTGCTGCGTCGTCAGAGCTTAGATGTAGAT 1444
DB      2006 ACTATGGTTATATTTTATATATTTCTGCTGCGTCGTCAGAGCTTAGATGTAGAT 2065
QY      1445 CTTTCCTTCTCTTTTGTGGGTAGATTTGAAATCCCTCAGCATTTGTCATCGGTAGTT 1504
DB      2066 CTTTCCTTCTCTTTTGTGGGTAGATTTGAAATCCCTCAGCATTTGTCATCGGTAGTT 2125
QY      1505 TTCTTTTCATGATTGTGACAAATGCAGCCTCGTGGGAGCTTTTGTAGGTAGA 1560
DB      2126 TTCTTTTCATGATTGTGACAAATGCAGCCTCGTGGGAGCTTTTGTAGGTAGA 2181

RESULT 9
US-09-068-101-5
; Sequence 5, Application US/09068101
; Patent No. 6372960
; GENERAL INFORMATION:
; APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Improved Barstar Gene
; FILE REFERENCE: 2121-139P
; CURRENT APPLICATION NUMBER: US/09/068,101
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: EP 9602446.9
; EARLIER FILING DATE: 1996-09-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4032
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: other nucleic
; OTHER INFORMATION: acid, "plasmid pmv71"
; FEATURE:
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; NAME/KEY: misc feature
; LOCATION: (1999)..(3400)
; OTHER INFORMATION: Label = PRA1, "promoter region of rice actin gene"
; OTHER INFORMATION: - contains an intron in the leader"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3401)..(3676)
; OTHER INFORMATION: Label = barstar, "Barstar DNA"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3677)..(4003)
; OTHER INFORMATION: Label = 3'nos, "region containing 3' untranslated
; OTHER INFORMATION: end of nopaline synthase gene of Agrobacterium"
; OTHER INFORMATION: T-DNA"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3399)..(3404)
; OTHER INFORMATION: Label = NcoI, "NcoI recognition site"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4016)..(4021)
; OTHER INFORMATION: Label = KpnI, "KpnI recognition site"
; US-09-068-101-5

Query Match      9.3%; Score 145; DB 3; Length 4032;
Best Local Similarity 100.0%; Pred. No. 1.4e-60;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1421 TGTGAGGCTTGAGATGCTAGATCTTTCTTTCTTTTGTGGTGAATTGAATCC 1480
DB      3259 TGTGAGGCTTGAGATGCTAGATCTTTCTTTCTTTTGTGGTGAATTGAATCC 3318
QY      1481 CTCAGCATGTCATCGTAGTATTTCTTTTCATGATTGTGACAAATGCAGCCTCGTGC 1540
DB      3319 CTCAGCATGTCATCGTAGTATTTCTTTTCATGATTGTGACAAATGCAGCCTCGTGC 3378
QY      1541 GGAAGCTTTTGTAGGTAGCAGCATG 1565
DB      3379 GGAAGCTTTTGTAGGTAGCAGCATG 3403

RESULT 10
US-09-970-921-5
; Sequence 5, Application US/0970921
; Patent No. 6759575
; GENERAL INFORMATION:
; APPLICANT: Frank Michiels et al.
; TITLE OF INVENTION: Improved Barstar Gene
; FILE REFERENCE: 2428-0108P
; CURRENT APPLICATION NUMBER: US/09/970,921
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4032
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: other nucleic
; OTHER INFORMATION: acid, "plasmid pmv71"
; NAME/KEY: misc feature
; LOCATION: (1999)..(3400)
; OTHER INFORMATION: Label = PRA1, "promoter region of rice actin gene"
; OTHER INFORMATION: - contains an intron in the leader"
; NAME/KEY: misc feature
; LOCATION: (3401)..(3676)
; OTHER INFORMATION: Label = barstar, "Barstar DNA"
; NAME/KEY: misc feature
; LOCATION: (3677)..(4003)
; OTHER INFORMATION: Label = 3'nos, "region containing 3' untranslated
; OTHER INFORMATION: end of nopaline synthase gene of Agrobacterium"
; OTHER INFORMATION: T-DNA"
; NAME/KEY: misc feature
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```
; LOCATION: (3399)..(3404) NCOI, "NCOI recognition site"  
; OTHER INFORMATION: label = NCOI  
; NAME/KEY: misc feature  
; LOCATION: (4016)..(4021)  
; OTHER INFORMATION: label = KpnI, "KpnI recognition site"  
; US-09-970-921-5
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Query Match	9.3%	Score 145	DB 4	Length 4032
Best Local Similarity	100.0%	Pred. NO.	1.4e-60	
Matches 145	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	1421	TCGTCAGGCTAGAGTGGTCAGATCTTCTCTCTCTTGTGGGTGAGATTGGAATCC	1480
Db	3359	TCGTCAGGCTAGAGTGGTCAGATCTTCTCTCTCTTGTGGGTGAGATTGGAATCC	3318
QY	1481	CTCAGCATGTTCAATCGGTAGTTTTCTTTTCATGATTTGGACAAATGCAAGCTCGTGC	1540
Db	3319	CTCAGCATGTTCAATCGGTAGTTTTCTTTTCATGATTTGGACAAATGCAAGCTCGTGC	3378

QY	1541	GGAGCTTTTGTAGGTAGC	1565
Db	3379	GGAGCTTTTGTAGGTAGC	3403

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RESULT 11
US-09-377-466B-19
; Sequence 19, Application US/09377466B
; Patent No. 6501009
;
; GENERAL INFORMATION:
;
; APPLICANT: Romano, Charles P.
;
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
;
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
;
; CURRENT APPLICATION NUMBER: US/09/377,466B
;
; CURRENT FILING DATE: 1999-08-19
;
; NUMBER OF SEQ ID NOS: 43
;
; SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 19

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? ORGANISM: Artificial Sequence
?
? FEATURE:
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? OTHER INFORMATION: Description of Artificial Sequence: expression
?
? OTHER INFORMATION: cassette
?
? NAME/KEY: Promoter
?
? LOCATION: (14)..(235)
?
? OTHER INFORMATION: P-CMV,AS4
?
? NAME/KEY: 5' UTR
?
? LOCATION: (240)..(304)
?
? OTHER INFORMATION: L-Ta.hcb1
?
? NAME/KEY: Intron
?
? LOCATION: (318)..(805)
?
? OTHER INFORMATION: I-Os.Act1
?
? NAME/KEY: CDS
?
? LOCATION: (811)..(2769)
?
? OTHER INFORMATION: Cyt3Bb1 variant 11231mv1
?
? NAME/KEY: terminator
?
? LOCATION: (2787)..(3020)
?
? OTHER INFORMATION: T-Ta.hep17
?
? JS-09-377-466B-19

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	Query Match	8.9%	Score 140;	DB 4;	Length 3039;
	Best Local Similarity	100.0%	Pred. No. 3e-58;		
	Matches 140;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1421	TCGTCAGGCTAGAGTGTCTAGATCTTCTCTCTCTTTGTGGGTGAAATTTGAATCC	1480		
Db	660	TCGTCAGGCTAGAGTGTCTAGATCTTCTCTCTTTGTGGGTGAAATTTGAATCC	719		
QY	1481	CTCAGCATTTGCATTCGGTAGTTTTCTTTTCATGATTTGACAAATGACCTCGTGC	1540		
Db	720	CTCAGCATTTGCATTCGGTAGTTTTCTTTTCATGATTTGACAAATGACCTCGTGC	779		
QY	1541	GGAGCTTTTGTGTAGTAGA	1560		

Db 780 GGAGCTTTTGTAGTAGA 799

RESULT 12  
US-09-377-466B-21  
; Sequence 21, Application US/09377466B

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; NUMBER OF SEQ ID NOS. 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21

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: TYPE: DNA
:
: ORGANISM: Artificial Sequence
:
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: expression

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? LOCATION: (14)..(235)
? OTHER INFORMATION: P-CAMP.AS4
? NAME/KEY: 5' UTR
? LOCATION: (240)..(304)
? OTHER INFORMATION: L-Ta.hcb1
? NAME/KEY: Intron
? LOCATION: (318)..(805)
? OTHER INFORMATION: I-08.Act1
? NAME/KEY: CDS
? LOCATION: (811)..(2769)
? OTHER INFORMATION: Cyt3BBD1 variant 11231mv2
? NAME/KEY: terminator
? LOCATION: (2787)..(3020)
? OTHER INFORMATION: T-Ta.hsp17
? US-09-377-466B-21

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Query Match 8.9%; Score 140; DB 4; Length 3039;  
Best Local Similarity 100.0%; Pred. No. 3.9e-58;  
Matches 140; Conservative 0; Mismatches 0; Indels

QY	1421	TCGTCAGGCTTAAGATGTCGATGATCTTCTCTCTCTTTTGTGGGAGAGATTTGAATCC	1480
QY	660	TCGTCAGGCTTAAGATGTCGATCTTCTCTCTCTTTTGTGGGAGAGATTTGAATCC	719
Db	1481	CTCAGCATTGTTCTACGCGTAGTTTCTTTTTCATGATTTTGTGACAAATGCAGCCTCGTC	1540
QY	720	CTCAGCATTGTTCTACGCGTAGTTTCTTTTTCATGATTTTGTGACAAATGCAGCCTCGTC	779

QY	1541	GGAGCTTTTGTAGGTAGA	1560
Db	780	GGAGCTTTTGTAGGTAGA	799

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RESULT 13
US-09-377-466B-38
; Sequence 38, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 3044
; TYPE: DNA
; ORGANISM: Artificial Sequence

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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: expression
OTHER INFORMATION: cassette
NAME/KEY: Promoter
LOCATION: (14)..(235)
OTHER INFORMATION: P-CMV.AS4
NAME/KEY: 5'UTR
LOCATION: (240)..(304)
OTHER INFORMATION: L-Ta.hcb1
NAME/KEY: Intron
LOCATION: (318)..(805)
OTHER INFORMATION: I-Os.Act1
NAME/KEY: CDS
LOCATION: (811)..(2769)
OTHER INFORMATION: variant Cry3Bb1 coding sequence encoding v11231
NAME/KEY: terminator
LOCATION: (2752)..(3025)
OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-38

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	Query Match	8.9%	Score 140;	DB 4;	Length 3044;
	Best Local Similarity	100.0%	Pred. No. 3.9e-58;		
	Matches 140;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Oy	1421	TCGTCAGGCTAGAGTGTCTAGATTTTCTTCTTTTGTGGTGAATTTGAATCC	1480		
Db	660	TCGTCAGGCTTAGATGTCTAGATTTTCTTCTTTTGTGGTGAATTTGAATCC	719		
Oy	1481	CTCAGCATTTGTCATCGGTAGTTTTCTTTTCATGATTTGTGCAAAATGACGCTCGTC	1540		
Db	720	CTCAGCATTTGTCATCGGTAGTTTTCTTTTCATGATTTGTGCAAAATGACGCTCGTC	779		
Oy	1541	GGAGCTTTTTTGTAAGTAGA	1560		
Db	780	GGAGCTTTTTTGTAAGTAGA	799		

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RESULT 14
US-09-377-466B-17
Sequence 17, Application US/09377466B
Patent No. 6501009
GENERAL INFORMATION:
APPLICANT: Romano, Charles P.
TITLE OR INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
FILE REFERENCE: 38-21(13504) Cry3Bb Improved Exp. Corn
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 3450
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: expression
OTHER INFORMATION: cassette
NAME/KEY: promoter
LOCATION: (14)..(235)
OTHER INFORMATION: P-CaMV.AS4
NAME/KEY: 5'UTR
LOCATION: (240)..(304)
OTHER INFORMATION: L-Ta.hcd1
NAME/KEY: intron
LOCATION: (316)..(805)
OTHER INFORMATION: I-Os.Act1
NAME/KEY: transic peptide
LOCATION: (825)..(971)
OTHER INFORMATION: amino terminal TS-Zm.rbcS
NAME/KEY: intron
LOCATION: (972)..(1134)
OTHER INFORMATION: I-Zm.rbcS
NAME/KEY: transic peptide
LOCATION: (1135)..(1221)

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? OTHER INFORMATION: carboxy terminus TS-2m.rbcs
? NAME/KEY: CDS
? LOCATION: (1222)..(3180)
? OTHER INFORMATION: Cy3bb1 variant 11231mv1
? NAME/KEY: terminator
? LOCATION: (3198)..(3431)
? OTHER INFORMATION: T-Ta.hsp17
? US-09-377-4668-17

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	Query Match	8.9%;	Score 140;	DB 4;	Length 3450;
	Best Local Similarity	100.0%;	Prod. No. 3.9e-58;		
	Matches 140;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1421	TCGTCAGGCTTAGATGTCGATGCTTCTCTCTTTTGTGCGGTAGATTGAATCC			1480
Db	660	TCGTCAGGCTTAGATGTCGATGCTTCTCTCTTTTGTGCGGTAGATTGAATCC			719
Qy	1481	CTCAGCATTTGTCATCGGTAGTTTCTTTTCATGATTTGTGCAAAATGCAGCCTCGTGC			1540
Db	720	CTCAGCATTTGTCATCGGTAGTTTCTTTTCATGATTTGTGCAAAATGCAGCCTCGTGC			779
Qy	1541	GGAGCTTTTGTAGGTAGA	1560		
Db	780	GGAGCTTTTGTAGGTAGA	799		

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1 RESULT 15
2 US-09-377-466B-36
3 ; Sequence 36, Application US/09377466B
4 ; Patent No. 6501009
5 ; GENERAL INFORMATION:
6 ; APPLICANT: Romano, Charles P.
7 ; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
8 ; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
9 ; CURRENT APPLICATION NUMBER: US/09/377,466B
10 ; CURRENT FILING DATE: 1999-08-19
11 ; NUMBER OF SEQ ID NOS: 43
12 ; SOFTWARE: PatentIn Ver. 2.0
13 SEQ ID NO 36
14 ;
15 ; LENGTH: 3455
16 ;
17 ; TYPE: DNA
18 ;
19 ; ORGANISM: Artificial Sequence
20 ; FEATURE:
21 ; OTHER INFORMATION: Description of Artificial Sequence: expression
22 ; OTHER INFORMATION: cassette
23 ;
24 ; NAME/KEY: Promoter
25 ; LOCATION: (14)..(235)
26 ; OTHER INFORMATION: P.CamV.AS4
27 ; NAME/KEY: 5'UTR
28 ; LOCATION: (240)..(304)
29 ; OTHER INFORMATION: L-Ta.hcb1
30 ; NAME/KEY: Intron
31 ; LOCATION: (318)..(805)
32 ; OTHER INFORMATION: I-Os.Act1
33 ; NAME/KEY: translat_peptide
34 ; LOCATION: (825)..(971)
35 ; OTHER INFORMATION: TS-2m.rbcs amino terminal coding sequence upstream
36 ; OTHER INFORMATION: of Zea mays rbcs Intron
37 ; NAME/KEY: Intron
38 ; LOCATION: (972)..(1134)
39 ; OTHER INFORMATION: I-2m.rbcs
40 ; NAME/KEY: translat_peptide
41 ; LOCATION: (1135)..(1221)
42 ; OTHER INFORMATION: TS-2m.rbcs carboxy terminus coding sequence
43 ; OTHER INFORMATION: downstream of Zea mays rbcs Intron
44 ; NAME/KEY: CDS
45 ; LOCATION: (1222)..(3180)
46 ; OTHER INFORMATION: variant Cry3Bb1 coding sequence encoding v11231
47 ; NAME/KEY: terminator
48 ; LOCATION: (3198)..(3431)
49 ; OTHER INFORMATION: T-Ta.hsp17
50 US-09-377-466B-36

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 11:40:58 ; Search time 830.171 Seconds  
(without alignments)  
12360.260 Million cell updates/sec

Title: US-10-758-799-3

Perfect score: 1565  
Sequence: 1 GAATTCCTCAGAGTCACGCG.....TTTTTGTAGTAGACCAAG 1565

Scoring table: OLIGO NUC  
Gap 60.0, Gapext 60.0

Searched: 7351250 seqs, 3283620254 residues

Word size : 0

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA.\*

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4	1021	65.2	1021	19	US-10-758-799-1
5	454	29.0	454	9	US-09-037-531-2
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7	296	18.9	623	9	US-09-981-900B-19

8	294	18.8	470	16	US-10-087-167-109	Sequence 109, App
9	236	15.1	1259	10	US-09-991-209-43	Sequence 43, App1
10	236	15.1	4773	10	US-09-991-209-32	Sequence 32, App1
11	236	15.1	4950	10	US-09-991-209-34	Sequence 34, App1
12	236	15.1	4965	10	US-09-991-209-37	Sequence 37, App1
13	236	15.1	4974	10	US-09-991-209-35	Sequence 35, App1
14	236	15.1	5164	10	US-09-991-209-36	Sequence 36, App1
15	236	15.1	5277	10	US-09-991-209-25	Sequence 25, App1
16	236	15.1	5395	10	US-09-991-209-38	Sequence 38, App1
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19	236	15.1	5337	10	US-09-991-209-23	Sequence 23, App1
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21	236	15.1	5338	10	US-09-991-209-15	Sequence 15, App1
22	236	15.1	5338	10	US-09-991-209-29	Sequence 29, App1
23	236	15.1	5345	10	US-09-991-209-17	Sequence 17, App1
24	236	15.1	5387	10	US-09-991-209-41	Sequence 41, App1
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26	145	9.3	2480	21	US-10-678-588A-1	Sequence 1, App1
27	145	9.3	4032	9	US-09-970-921-5	Sequence 5, App1
28	145	9.3	5365	22	US-10-839-092-57	Sequence 57, App1
29	145	9.3	7943	10	US-09-845-064-15	Sequence 15, App1
30	145	9.3	9143	10	US-09-845-064-12	Sequence 12, App1
31	145	9.3	10003	10	US-09-845-064-21	Sequence 21, App1
32	142	9.1	9359	21	US-10-344-977A-1	Sequence 1, App1
33	142	9.1	9359	22	US-10-344-975B-1	Sequence 1, App1
34	141	9.0	6865	10	US-09-845-064-13	Sequence 13, App1
35	141	9.0	10003	10	US-09-845-064-21	Sequence 21, App1
36	140	8.9	491	9	US-09-376-940-50	Sequence 50, App1
37	140	8.9	1597	22	US-10-839-092-50	Sequence 50, App1
38	140	8.9	3034	20	US-10-841-796-34	Sequence 34, App1
39	140	8.9	3039	15	US-10-232-665-19	Sequence 19, App1
40	140	8.9	3039	15	US-10-232-665-21	Sequence 21, App1
41	140	8.9	3044	15	US-10-232-665-17	Sequence 17, App1
42	140	8.9	3450	15	US-10-232-665-36	Sequence 36, App1
43	140	8.9	3455	15	US-10-232-665-23	Sequence 23, App1
44	140	8.9	3469	15	US-10-232-665-23	Sequence 23, App1
45	140	8.9	7794	24	US-11-057-062-2	Sequence 2, App1

#### ALIGNMENTS

RESULT 1  
US-09-037-531-3  
; Sequence 3, Application US/09037531  
; Patent No. US20020104117A1  
; GENERAL INFORMATION:  
; APPLICANT: DeRose, Richard  
; TITLE OF INVENTION: Freysinet, Georges  
; TITLE OF INVENTION: Maize H3C4 Promoter Combined With The  
; TITLE OF INVENTION: First Intron Of Rice Actin, Chimeric Gene Comprising It  
; TITLE OF INVENTION: And Transformed Plant  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Connolly, Bove, Lodge, & Hutz  
; STREET: 1220 Market Street  
; CITY: Wilmington  
; STATE: DE  
; COUNTRY: USA  
; ZIP: 19899  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/037, 531  
; FILING DATE: 10-MAR-1998  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMorris Jr., Robert G.  
; REGISTRATION NUMBER: 30962

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REFERENCE/DOCKET NUMBER: 5500*24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302)658-9141
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1565 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-037-531-3

Query Match      100.0%; Score 1565; DB 9; Length 1565;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAATTCCTGACAGTCGACGAGTCCCTTATGTGACCAATTACGTAAATGCAATCAT
DB      1 GAATTCCTGACAGTCGACGAGTCCCTTATGTGACCAATTACGTAAATGCAATCAT
QY      61 TTAATTTGAATAGAACTTTTCTATATATCTTTACTTAACATATCTTGTTTAAAT
DB      61 TTAATTTGAATAGAACTTTTCTATATATCTTTACTTAACATATCTTGTTTAAAT
QY      121 TCAGTCTCAACATTCATTGCTCAAGTATAGTTGAGACTGTCAAAATTTACTATTTAT
DB      121 TCAGTCTCAACATTCATTGCTCAAGTATAGTTGAGACTGTCAAAATTTACTATTTAT
QY      181 TTCTTCATATTTTTTTTCTTATACACATTTTGCGCTTACATCATATATATCA
DB      181 TTCTTCATATTTTTTTTCTTATACACATTTTGCGCTTACATCATATATATCA
QY      241 TCCCTTCGCGTGCCTCTAAAGATTCACATCCCTCAATCTTATCTCTCCAAATACGT
DB      241 TCCCTTCGCGTGCCTCTAAAGATTCACATCCCTCAATCTTATCTCTCCAAATACGT
QY      301 TCTCTAAATCAGGTCTCTATAGCAATACCTATATTTAGAGACATTTTTTATTTTGTAC
DB      301 TCTCTAAATCAGGTCTCTATAGCAATACCTATATTTAGAGACATTTTTTATTTTGTAC
QY      361 ATACATATTTTGTCTACTCTCAATGCAATATATCATATTTAGTTTACTTAAACCGATTAT
DB      361 ATACATATTTTGTCTACTCTCAATGCAATATATCATATTTAGTTTACTTAAACCGATTAT
QY      421 TTTAAATATTCAGAGGAGAGAACTGTTTATATTTCTATATATAGAGATCCAGT
DB      421 TTTAAATATTCAGAGGAGAGAACTGTTTATATTTCTATATATAGAGATCCAGT
QY      481 AGCGTTCTCTAAATTTAGATGATTTATTTAGAGAGCGCTGTTAGAAAACGTAAAAATTCG
DB      481 AGCGTTCTCTAAATTTAGATGATTTATTTAGAGAGCGCTGTTAGAAAACGTAAAAATTCG
QY      541 TTGATTTATTTATATTTAGGATAGAGTACCTTTATGCTTTATATAGATCTTTGTGACCA
DB      541 TTGATTTATTTATATTTAGGATAGAGTACCTTTATGCTTTATATAGATCTTTGTGACCA
QY      601 GCGTTTACCGGTTATTTTCGGAATGCGGCTCTCAATTTTCACTCCAGGCCCCCAATTT
DB      601 GCGTTTACCGGTTATTTTCGGAATGCGGCTCTCAATTTTCACTCCAGGCCCCCAATTT
QY      661 TCACGTTTTCACGGAAGCGCCAGCTGCTTAACCAAAATTTGTAAGGTGCGCGGTT
DB      661 TCACGTTTTCACGGAAGCGCCAGCTGCTTAACCAAAATTTGTAAGGTGCGCGGTT
QY      721 TTTCAAAAGAAGTGGAAACCATCTGACCCAGACTAGTAGGCGCTCGGATCTCTCCG
DB      721 TTTCAAAAGAAGTGGAAACCATCTGACCCAGACTAGTAGGCGCTCGGATCTCTCCG
QY      781 ATTAAGTCTAGGCAATAGAGAGCCCAACCAACCATCAAGCGGATGCTCCCAAGCTTC
DB      781 ATTAAGTCTAGGCAATAGAGAGCCCAACCAACCATCAAGCGGATGCTCCCAAGCTTC
QY      841 CACCTCATGGGCGCGTCCATCTCCATCCAAACCTATTCGTTACCTTGCCCATCTCC
DB      841 CACCTCATGGGCGCGTCCATCTCCATCCAAACCTATTCGTTACCTTGCCCATCTCC
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DB      841 CACCTCATGGGCGCGTCCATCTCCATCCAAACCTATTCGTTACCTTGCCCATCTCC
QY      901 GAAAAAATTTCTGGGTCCGCTCCGACCTTCTAATAATCCATCCATACAGCGGAT
DB      901 GAAAAAATTTCTGGGTCCGCTCCGACCTTCTAATAATCCATCCATACAGCGGAT
QY      961 CGCATCACTGCAAAATCCCGAGAAATCAACACCTCCCAATTTCCAGCTGCAACCACT
DB      961 CGCATCACTGCAAAATCCCGAGAAATCAACACCTCCCAATTTCCAGCTGCAACCACT
QY      1021 CGCGGTCTCTCGCGCAAGACCAAAAGAAATTTGCGCCACCGCGGTGAGTCTCTCCC
DB      1021 CGCGGTCTCTCGCGCAAGACCAAAAGAAATTTGCGCCACCGCGGTGAGTCTCTCCC
QY      1081 CTTCCCGCTCCGCGCGCGCGCGGTAAACACCCCGCCCTCTCTCTTTCTTTCTCGGTTT
DB      1081 CTTCCCGCTCCGCGCGCGCGCGGTAAACACCCCGCCCTCTCTCTTTCTTTCTCGGTTT
QY      1141 TTTTTCGTCTGATCTGATCTTTGATCTTTGATTTGAGTGGGCGAGAGCGGCTTCG
DB      1141 TTTTTCGTCTGATCTGATCTTTGATCTTTGATTTGAGTGGGCGAGAGCGGCTTCG
QY      1201 TCGCCCAAGTCGATCGCGGAGGCGGAGATCTCGCGGCTGCGCTTCGCGGCTGAGT
DB      1201 TCGCCCAAGTCGATCGCGGAGGCGGAGATCTCGCGGCTGCGCTTCGCGGCGTGAAT
QY      1261 CGGCGCGGATCTCGCGGAGGAGATGGGGCTCTCGAGATGATCTGATCGCGGCTGTTGG
DB      1261 CGGCGCGGATCTCGCGGAGGAGATGGGGCTCTCGAGATGATCTGATCGCGGCTGTTGG
QY      1321 GGGGAGATGATGGGGGTTTAAATTTCCCATGCTTAAACAGATCAGAGAGAGGAGAAA
DB      1321 GGGGAGATGATGGGGGTTTAAATTTCCCATGCTTAAACAGATCAGAGAGAGGAGAAA
QY      1381 GGGGAGATGATGGGGGTTTAAATTTCCCATGCTTAAACAGATCAGAGAGAGGAGAAA
DB      1381 GGGGAGATGATGGGGGTTTAAATTTCCCATGCTTAAACAGATCAGAGAGAGGAGAAA
QY      1441 AGATCTTCTTCTCTCTTTTGTGGGTGAATTTGAATCCCGACAGATTTGATCGGTA
DB      1441 AGATCTTCTTCTCTCTTTTGTGGGTGAATTTGAATCCCGACAGATTTGATCGGTA
QY      1501 GTTTTCTTCTTATATTTGTAACAATGACAGCTCTGTCGCGAGCTTTTGTAGTAGA
DB      1501 GTTTTCTTCTTATATTTGTACAAATGACAGCTCTGTCGCGAGCTTTTGTAGTAGA
QY      1561 CCATG 1565
DB      1561 CCATG 1565

RESULT 2
US-10-758-799-3
; Sequence 3, Application US/10758799
; Publication No. US20040199944A1
; GENERAL INFORMATION:
; APPLICANT: Dekose, Richard
; Freysinet, Georges
; TITLE OF INVENTION: Maize H3C4 Promoter Combined With The
; Fixed Intron Of Rice Actin, Chimeric Gene Comprising It
; And Transformed Plant
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/758, 799  
FILING DATE: 16-Jan-2004  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/037, 531  
FILING DATE: 10-MAR-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: McMorrow Jr., Robert G.  
REGISTRATION NUMBER: 30962  
REFERENCE/DOCKET NUMBER: 5500\*24  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302)658-9141  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1565 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-758-799-3

Query Match 100.0%; Score 1565; DB 19; Length 1565;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCCTGAGGTCGACGATCCCTTATGTCACCATTTCTGATGATGATATCAT 60  
DB 1 GAATTCCTGAGGTCGACGATCCCTTATGTCACCATTTCTGATGATGATATCAT 60  
QY 61 TTAATGATAGCAAACTTTCTATTACTTTCTTACTACATTAATTCGTTTAAAT 120  
DB 61 TTAATGATAGCAAACTTTCTATTACTTTCTTACTACATTAATTCGTTTAAAT 120  
QY 121 TCAAGTCTCAACATTCATGCTCAAGTAAAGTTGAGACCTGTCMAAATTTACTATTTTAT 180  
DB 121 TCAAGTCTCAACATTCATGCTCAAGTAAAGTTGAGACCTGTCMAAATTTACTATTTTAT 180  
QY 181 TTCTCATATTTTTCCTTATACATATTTGGGCTTACATTCATCTATATATCCA 240  
DB 181 TTCTCATATTTTTCCTTATACATATTTGGGCTTACATTCATCTATATATCCA 240  
QY 241 TCCCTTCGCGTCTCTTAAAGATTCATCTCTGAATCTTATTCCTCTCAATAAGCT 300  
DB 241 TCCCTTCGCGTCTCTTAAAGATTCATCTCTGAATCTTATTCCTCTCAATAAGCT 300  
QY 301 TCTCTAATCAGGTCCTATAGCAATCACTATATTAAGACATTTTATTTTGTAC 360  
DB 301 TCTCTAATCAGGTCCTATAGCAATCACTATATTAAGACATTTTATTTTGTAC 360  
QY 361 ATATCATTTTGTCACTCTCAATGATATATATATTTAGTTTACTTAAACGATAT 420  
DB 361 ATATCATTTTGTCACTCTCAATGATATATATATTTAGTTTACTTAAACGATAT 420  
QY 421 TTAAGATTCMAACGATGAAAGATGTTAGTAATTTCTATATTAAGAGATCCAGT 480  
DB 421 TTAAGATTCMAACGATGAAAGATGTTAGTAATTTCTATATTAAGAGATCCAGT 480  
QY 481 AGCGTCTCTAAATTTAGATGATATTTAGAGAGCGCTGTAGAAAACGTAAAAATTC 540  
DB 481 AGCGTCTCTAAATTTAGATGATATTTAGAGAGCGCTGTAGAAAACGTAAAAATTC 540  
QY 541 TTGATTTATTAATTTTGGGAGTAGCCCTTATATGCTTATATATTTTGGTGAACCA 600  
DB 541 TTGATTTATTAATTTTGGGAGTAGCCCTTATATGCTTATATATTTTGGTGAACCA 600  
QY 601 GCCTTATACGGTATTTTGGCGATTCGCGCTCATTTTCACTCCAGCCGCCACATTT 660  
DB 601 GCCTTATACGGTATTTTGGCGATTCGCGCTCATTTTCACTCCAGCCGCCACATTT 660

QY 661 TCAGTTTTCAAGGAGCGCCAGCGCTGCTATACCAAAATTTGTACGGTGGCGGTT 720  
DB 661 TCAGTTTTCAAGGAGCGCCAGCGCTGCTATACCAAAATTTGTACGGTGGCGGTT 720  
QY 721 TTCAAAAGAGTTCGGAACCATCTGACCCACCGACTAGTAGGCGCTCGGATCTCCCT 780  
DB 721 TTCAAAAGAGTTCGGAACCATCTGACCCACCGACTAGTAGGCGCTCGGATCTCCCT 780  
QY 781 ATTAAGTCTTACGCAATTAAGAGCCGCAACCACTTACGCGGATTCGCTTACGCTTC 840  
DB 781 ATTAAGTCTTACGCAATTAAGAGCCGCAACCACTTACGCGGATTCGCTTACGCTTC 840  
QY 841 CACCTATGCGGCGCGCTTCACTTCAACCACTTATTCGTTACCTTGGCCATCTCC 900  
DB 841 CACCTATGCGGCGCGCTTCACTTCAACCACTTATTCGTTACCTTGGCCATCTCC 900  
QY 901 GAAAAAATTCGCGCTTCGCGCTCCGACCTACTACAAATACCATCCATCAAGACGAT 960  
DB 901 GAAAAAATTCGCGCTTCGCGCTCCGACCTACTACAAATACCATCCATCAAGACGAT 960  
QY 961 CGCATCACTGCAAAATCCCGCAAAATCAACACTTCCCAATTCACGCTGCCACCACT 1020  
DB 961 CGCATCACTGCAAAATCCCGCAAAATCAACACTTCCCAATTCACGCTGCCACCACT 1020  
QY 1021 CGCGCTCTCCGCGCGGCGGACCAAGAAATTTGGCCGACCGCGGTGAGCTCTCC 1080  
DB 1021 CGCGCTCTCCGCGCGGCGGACCAAGAAATTTGGCCGACCGCGGTGAGCTCTCC 1080  
QY 1081 CTCCCGCTCCGCGCGGCGGACCAAGAAATTTGGCCGACCGCGGTGAGCTCTCC 1140  
DB 1081 CTCCCGCTCCGCGCGGCGGACCAAGAAATTTGGCCGACCGCGGTGAGCTCTCC 1140  
QY 1141 TTTTTCGTCGCTCGATCTGATCTTTGAGCTTGGAGTGGGCGAGAGCGGCTTCG 1200  
DB 1141 TTTTTCGTCGCTCGATCTGATCTTTGAGCTTGGAGTGGGCGAGAGCGGCTTCG 1200  
QY 1201 TCGCCCAAGATCGGTGGCGGAGAGGGCGGATCTTCGCGGTGGCTCTCCGGCGCTGAGT 1260  
DB 1201 TCGCCCAAGATCGGTGGCGGAGAGGGCGGATCTTCGCGGTGGCTCTCCGGCGCTGAGT 1260  
QY 1261 CGGCGCGGATTCCTCGCGGGAATGAGGCTCTCGGATGATGATCTGATCCGCGTGTGG 1320  
DB 1261 CGGCGCGGATTCCTCGCGGGAATGAGGCTCTCGGATGATGATCTGATCCGCGTGTGG 1320  
QY 1321 GGGAGATGATGAGGCGCTTAAATTTGCGCATCTTAAACAGATCAAGAAAGGGAATA 1380  
DB 1321 GGGAGATGATGAGGCGCTTAAATTTGCGCATCTTAAACAGATCAAGAAAGGGAATA 1380  
QY 1381 GGGCATATGCTTATATTTTATATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440  
DB 1381 GGGCATATGCTTATATTTTATATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440  
QY 1441 AGATCTTCTCTCTCTCTTTTGGGAGTAGAATTTGAATCCCTGAGATTTTATCGGTA 1500  
DB 1441 AGATCTTCTCTCTCTTTTGGGAGTAGAATTTGAATCCCTGAGATTTTATCGGTA 1500  
QY 1501 GTTTTCTTTTCAATGATTTTGTGCAAAATGACGCTGCGGAGCTTTTGTAGGTAGA 1560  
DB 1501 GTTTTCTTTTCAATGATTTTGTGCAAAATGACGCTGCGGAGCTTTTGTAGGTAGA 1560  
QY 1561 CCATG 1565  
DB 1561 CCATG 1565

RESULT 3  
US-09-037-531-1  
Sequence 1, Application US/09037531  
Patent No. US20020104117A1  
GENERAL INFORMATION:  
APPLICANT: DeRose, Richard  
APPLICANT: Freydsine, Georges  
TITLE OF INVENTION: Maize H3C4 Promoter Combined With The

TITLE OF INVENTION: First Intron Of Rice Actin, Chimeric Gene Comprising It  
TITLE OF INVENTION: And Transformed Plant  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Connolly, Bove, Lodge, & Hutz  
STREET: 1220 Market Street  
CITY: Wilmington  
STATE: DE  
COUNTRY: USA  
ZIP: 19899  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/037,531  
FILING DATE: 10-MAR-1998  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: McMorrow Jr., Robert G.  
REGISTRATION NUMBER: 30962  
REFERENCE/DOCKET NUMBER: 5500\*24  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302)658-9141  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1021 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-037-531-1

Query Match 65.2%; Score 1021; DB 9; Length 1021;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1021; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

27 CTTATGTGACCCCTTATCTGATATGATATCATATTTATGATAGAACTTTCTATT 86  
1 CTTATGTGACCCCTTATCTGATATGATATCATATTTATGATAGAACTTTCTATT 60  
87 ACTCTTTTACTACATATATCTGTTTAAATTCAGTCCCTCAACATTCATTGCTCAAG 146  
61 ACTCTTTTACTACATATATCTGTTTAAATTCAGTCCCTCAACATTCATTGCTCAAG 120  
147 TATAGTGGAGCTGTCAAAATTTACTATTTTATTTCTTCATATTTTTCCTTAACA 206  
121 TATAGTGGAGCTGTCAAAATTTACTATTTTATTTCTTCATATTTTTCCTTAACA 180  
207 CATTTTGGGCTTACATCATATCTATATCCATCTTCCGGTGTCTCTTAAAGATT 266  
181 CATTTTGGGCTTACATCATATCTATATCCATCTTCCGGTGTCTCTTAAAGATT 240  
267 CCATCCCTGATCTTATCTCTCCCAATAGCTTCTTAATCAGGCTCTTAAGCAA 326  
241 CCATCCCTGATCTTATCTCTCCCAATAGCTTCTTAATCAGGCTCTTAAGCAA 300  
327 TACCTATATTAGAGACATTTTATTTTGTACATACATATTTGTCTCAATG 386  
301 TACCTATATTAGAGACATTTTATTTTGTACATACATATTTGTCTCAATG 360  
387 CATTATACATATTGTTTGTACAAACCATTTATTTAAATTTTCAACGGAAGAAAC 446  
361 CATTATACATATTGTTTGTACAAACCATTTATTTAAATTTTCAACGGAAGAAAC 420  
447 TGTTTAGATTAATTTCTATATATAGAGATCCAGTAGGCTCTCAATTTAGATGATAT 506  
421 TGTTTAGATTAATTTCTATATATAGAGATCCAGTAGGCTCTCAATTTAGATGATAT 480  
507 TTAGAGAGCGCTGTAGAAACGTAAGAAATTTCTTTGATTATTTATTTAGGCTAGAT 566  
481 TTAGAGAGCGCTGTAGAAACGTAAGAAATTTCTTTGATTATTTATTTAGGCTAGAT 540

567 ACCCTTATGCTTTATAGATCTTTGTGAGACCCAGCTTATACGGTTATTTTCCGATT 626  
541 ACCCTTATGCTTTATAGATCTTTGTGAGACCCAGCTTATACGGTTATTTTCCGATT 600  
627 GCGCTCTCATTTTCACTTCAGAGCCGCCACATTTTCAAGTTTTCACCGAAGGCCAGCC 686  
601 GCGCTCTCATTTTCACTTCAGAGCCGCCACATTTTCAAGTTTTCACCGAAGGCCAGCC 660  
687 TGCCTAACCAAAATTTGTACGATGCGCGGCTTTTCAAGAAAGATCGGAAACCATCTGC 746  
661 TGCCTAACCAAAATTTGTACGATGCGCGGCTTTTCAAGAAAGATCGGAAACCATCTGC 720  
747 ACCCAACGACTGTAGAGCCCTCGATCTCTCCCTGATTAAGTCTTACCAATAGAGCCCA 806  
721 ACCCAACGACTGTAGAGCCCTCGATCTCTCCCTGATTAAGTCTTACCAATAGAGCCCA 780  
807 GAACCAACCATGACGCGGATCGCTTCAAGCTTCACTCATGAGCGCGCTCATCTCCA 866  
781 GAACCAACCATGACGCGGATCGCTTCAAGCTTCACTCATGAGCGCGCTCATCTCCA 840  
867 TCCACACCTATTTCCGTTACCTTGCACATCCCTCGAATAAATTCGCGTGGCGCTCGC 926  
841 TCCACACCTATTTCCGTTACCTTGCACATCCCTCGAATAAATTCGCGTGGCGCTCGC 900  
927 ACTCTACAAATTAACCATCCCATCCATCAGACGATGCACTGCAATCCCGAGAA 986  
901 ACTCTACAAATTAACCATCCCATCCATCAGACGATGCACTGCAATCCCGAGAA 960  
987 ATCAACACCTCCCAATTTCCAGCTGCGCAACCACTGCGGCTCTCGCGCAACCA 1046  
961 ATCAACACCTCCCAATTTCCAGCTGCGCAACCACTGCGGCTCTCGCGCAACCA 1020

1047 G 1047  
1021 G 1021

RESULT 4  
US-10-758-799-1  
Sequence 1, Application US/10758799  
Publication No. US2004019944A1  
GENERAL INFORMATION:  
APPLICANT: Derose, Richard  
Freysinet, Georges  
TITLE OF INVENTION: Maize H3C4 Promoter Combined With The  
First Intron Of Rice Actin, Chimeric Gene Comprising It  
And Transformed Plant  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Connolly, Bove, Lodge, & Hutz  
STREET: 1220 Market Street  
CITY: Wilmington  
STATE: DE  
COUNTRY: USA  
ZIP: 19899  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/758,799  
FILING DATE: 16-Jan-2004  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/037,531  
FILING DATE: 10-MAR-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: McMorrow Jr., Robert G.  
REGISTRATION NUMBER: 30962  
REFERENCE/DOCKET NUMBER: 5500\*24  
TELECOMMUNICATION INFORMATION:



```

1      TELEPHONE: (302)658-9141
2
3      INFORMATION FOR SEQ ID NO: 1:
4
5          SEQUENCE CHARACTERISTICS:
6
7              LENGTH: 1021 base pairs
8              TYPE: nucleic acid
9              STRANDEDNESS: single
10             TOPOLOGY: linear
11
12             MOLECULE TYPE: DNA (genomic)
13
14             SEQUENCE DESCRIPTION: SEQ ID NO: 1:
15
16     US-10-758-799-1

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Query Match	65.2%	Score 1021;	DB 19;	Length 1021;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1021; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

Qy	2	CTTATGAGCACTTATGATAGATAGATAATCATTTAATGAAATGCAAACTTTTCAAT	86
Db	1	CTTATGAGCACTTATGATAGATAGATAATCATTTAATGAAATGCAAACTTTTCAAT	60
Qy	87	ACTCTTTACTAACATAAATCTTGTTTTTAAATTCAGTCTCAACATTCATTCGTCAG	146
Db	61	ACTCTTTACTAACATAAATCTTGTTTTTAAATTCAGTCTCAACATTCATTCGTCAG	120
Qy	147	TATPAGTTGAGCTGTCAAAATTTACTATTTTATTTCTTCATATTTTTTTCCTTATCA	206
Db	121	TATPAGTTGAGCTGTCAAAATTTACTATTTTATTTCTTCATATTTTTTTCCTTATCA	180
Qy	207	CATTTGGGGCTACAAATCAATCATATCATATCTTCGCGGTCTCTAAAGATT	266
Db	181	CATTTGGGGCTACAAATCAATCATATCATATCTTCGCGGTCTCTAAAGATT	240
Qy	267	CCAATCCTGTAATCTTATTCCTCTCCAAATACGTTCTCTAAATCAGTCTCTATAGCAA	326
Db	241	CCAATCCTGTAATCTTATTCCTCTCCAAATACGTTCTCTAAATCAGTCTCTATAGCAA	300
Qy	327	TACCTATATTAGAACATTTTTTATTTTTTTGTACATACATATTTGTCATCTCAATG	386
Db	301	TACCTATATTAGAACATTTTTTATTTTTTTGTACATACATATTTGTCATCTCAATG	360
Qy	387	CATTATPACATTTAGTTTTTACTCAAAACGATTTATTAAGATTCAAAACGATTAAGAAC	446
Db	361	CATTATPACATTTAGTTTTTACTCAAAACGATTTATTAAGATTCAAAACGATTAAGAAC	420
Qy	447	TGTTTGAATTAATTTCTATATATPAGAAATCCAGTAGCGTCTCTAAATTTAGATGATTA	506
Db	421	TGTTTGAATTAATTTCTATATATPAGAAATCCAGTAGCGTCTCTAAATTTAGATGATTA	480
Qy	507	TTAGAGACGCTGTAGAAAACGTAAAAAATCTTTGATTTATTTATTTAGGGTAGAGT	566
Db	481	TTAGAGACGCTGTAGAAAACGTAAAAAATCTTTGATTTATTTATTTAGGGTAGAGT	540
Qy	567	AGCCTTATAGCTTTATATAGATCTTTGGTGAACCCAGCCTTATACCGGTTATTTTGGCAT	626
Db	541	AGCCTTATAGCTTTATATAGATCTTTGGTGAACCCAGCCTTATACCGGTTATTTTGGCAT	600
Qy	627	GCGCCTCTCATTTTCACTCGAGGCCCCCATTTTTCAAGTTTACGCAAGCGCCAGCC	686
Db	601	GCGCCTCTCATTTTCACTCGAGGCCCCCATTTTTCAAGTTTACGCAAGCGCCAGCC	660
Qy	687	TGCTTAACCAAAATTTGGTACGGTGGCGGGTTTTCAAAAGAAAGTCGGAACCATCTGC	746
Db	661	TGCTTAACCAAAATTTGGTACGGTGGCGGGTTTTCAAAAGAAAGTCGGAACCATCTGC	720
Qy	747	ACCCACGAGTACTAGAGCCCTCGGATCTCTCTCTGATTAAGTCTTAGGCCAATAGGAGCCCA	806
Db	721	ACCCACGAGTACTAGAGCCCTCGGATCTCTCTCTGATTAAGTCTTAGGCCAATAGGAGCCCA	780
Qy	807	GAACCAACCATCAACGGGATCGTCCCTTAGCTTCCACCTCATCGGCGCGTCCATCTCCA	866
Db	781	GAACCAACCATCAACGGGATCGTCCCTTAGCTTCCACCTCATCGGCGCGTCCATCTCCA	840
Qy	867	TCCAACACCTATTCGGTACCTTGCCCATCTTCGAAAAAATTTCTCGGCTCGGCTCGC	926

Db	841	TCCAACACCTATTCGGTTACCTTGCCATCCTCCGAAAAATTCGCGCTGGGCTCCG	900
QY	927	ACCTACTACAAATACCCATCCCATCAGAGCATGCATCATCTGCCAATATCCCCAGAA	986
Db	901	ACCTACTACAAATACCCATCCCATCAGAGCATGCATCATCTGCCAATATCCCCAGAA	960
QY	987	ATCAACACCTCCCAATTCAGCGCTGCCACCACTGCGCTCTCGGCGCAAGCACCAA	1046
Db	961	ATCAACACCTCCCAATTCAGCGCTGCCACCACTGCGCTCTCGGCGCAAGCACCAA	1020
QY	1047	G 1047	
Db	1021	G 1021	

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US-09-037-531-2          RESULT 5
Sequence 2, Application US/09037531
Patent No. US2002104117A1
GENERAL INFORMATION:
APPLICANT: DeRose, Richard
INVENTOR: Freysinet, Georges
TITLE OF INVENTION: Maize H3CA Promoter Combined With The
FIRST INTRON OF RICE ACTIN, CHIMERIC GENE COMPRISING IT
TITLE OF INVENTION: And Transformed Plant
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Connolly, Bove, Lodge, & Hutzel
STREET: 1220 Market Street
CITY: Wilmington
STATE: DE
COUNTRY: USA
ZIP: 19899
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037.531
FILING DATE: 10-MAR-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: McMorris Jr., Robert G.
REGISTRATION NUMBER: 30962
REFERENCE/DOCKET NUMBER: 5500*24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302)658-9141
INFORMATION FOR SEQ ID NO.: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-037-531-2

Query Match      29.0%; Score 454; DB 9; Length 454;
Best Local Similarity 100.0%; Pred. No. 3.8e+219;
Matches 454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY	1102	GAACACACCCGCCCCCTCTCCCTCTTCTTCTTCGCTTTTTCGCTCGGTCGCAT	1161
Db	1	GAACACACCCGCCCCCTCTCCCTCTTCTTCTTCGCTTTTTCGCTCGGTCGCAT	60
QY	1162	CTTTGGCCTTGATGTTGGTGGGCGAGACGGCTTCGTCGCCAGATCGATGGCGGG	1221
Db	61	CTTTGGCCTTGATGTTGGTGGGCGAGACGGCTTCGTCGCCAGATCGATGGCGGG	120
QY	1222	AGGGCGGGATCTCGCGGCTGACGCTCTCGGGCGTGAATCGGCGCCGATCTCTCGCGGGA	1281
Db	121	AGGGCGGGATCTCGCGGCTGACGCTCTCGGGCGGATCGAGCTCTCTCGCGGGA	180





```

Db      4603 CCGGGCGTGAATCGGGCCCGGATCTCGCGGGGAATCGGGCTCTCGATGTAGATCT 4658

RESULT 11
US-09-991-209-34
; Sequence 34, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 4950
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pJ06.1 vector
US-09-991-209-34

Query Match      15.1%; Score 236; DB 10; Length 4950;
Best Local Similarity 100.0%; Pred. No. 1.5e-108; Mismatches 0; Indels 0; Gaps 0;
Matches 236; Conservative 0;

Oy      1069 GAGCTCTCTCCCTCCCTCCGCGCGCGGTAACACCCCGCCTCTCTTTC 1128
Db      4600 GAGCTCTCTCCCTCCCTCCGCGCGCGGTAACACCCCGCCTCTCTTTC 4659

Oy      1129 TTTCTCGTTTTTTTTTTCGTCCTCGATCTTGTGCTTGGCTTGGGTGCGG 1188
Db      4660 TTTCTCGTTTTTTTTTTCGTCCTCGATCTTGTGCTTGGCTTGGGTGCGG 4719

Oy      1189 AGAGGGGCTTCCTCCCGCATCGGTGCGCGGAGGGAGGATCTCGGCGCTGCGTCT 1248
Db      4720 AGAGGGGCTTCCTCCCGCATCGGTGCGCGGAGGGAGGATCTCGGCGCTGCGTCT 4779

Oy      1249 CCGGCGTGAATCGGCGCGGATCTCTCGCGGGAATCGGGCTCTCGATGTAGATCT 1304
Db      4780 CCGGCGTGAATCGGCGCGGATCTCTCGGGAATCGGGCTCTCGATGTAGATCT 4835

RESULT 12
US-09-991-209-37
; Sequence 37, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 4965
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

```

```

: OTHER INFORMATION: pJQ3 vector
: US-09-991-209-37

Query Match      15.1%; Score 236; DB 10; Length 4965;
Best Local Similarity 100.0%; Pred. No. 1.5e-108;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1069 GAGCTCTCTCCCCCCTCCCTCCGCGCGCGCGGATACACCCCGCCCTCTCTCTTTC 1128
DB 504 GAGCTCTCTCCCCCCTCCCTCCGCGCGCGCGGATACACCCCGCCCTCTCTCTTTC 563
QY 1129 TTTCCTCGTTTTTTTTTTCGCTCGCTCTCGATCTTTGGCTTGGTAGTTGGGATGGGCG 1188
DB 564 TTTCCTCGTTTTTTTTTTCGCTCGCTCTCGATCTTTGGCTTGGTAGTTGGGATGGGCG 623
QY 1189 AGAGCGGCTTCGTGCGCCAGATCGGTGCGCGCGGAGCGCGGAGATCTCGCGCTGCGCTCT 1248
DB 624 AGAGCGGCTTCGTGCGCCAGATCGGTGCGCGCGGAGCGCGGAGATCTCGCGCTGCGCTCT 683
QY 1249 CCGGCGCTGAGTCCGCGCCCGGATCTTCGCGGCGGAGATGGGGCTCTCGGATGTAGATCT 1304
DB 684 CCGGCGCTGAGTCCGCGCCCGGATCTTCGCGGCGGAGATGGGGCTCTCGGATGTAGATCT 739

RESULT 13
US-09-991-209-35
: Sequence 35, Application US/09991209
: Publication No. US20030024009a1
: GENERAL INFORMATION:
: APPLICANT: Dunn-Coleman, Nigel
: APPLICANT: Langdon, Timothy
: APPLICANT: Morse, Phillip
: TITLE OF INVENTION: Manipulation of the Phenolic Acid
: TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
: TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
: FILE REFERENCE: GSC48-2
: CURRENT APPLICATION NUMBER: US/09/991,209
: CURRENT FILING DATE: 2002-07-02
: PRIOR APPLICATION NUMBER: US 60/249,608
: PRIOR FILING DATE: 2000-11-17
: NUMBER OF SEQ ID NOS: 97
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 35
: LENGTH: 4974
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: pJQ4 vector
: US-09-991-209-35

Query Match      15.1%; Score 236; DB 10; Length 4974;
Best Local Similarity 100.0%; Pred. No. 1.5e-108;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1069 GAGCTCTCTCCCCCCTCCCTCCGCGCGCGCGGATACACCCCGCCCTCTCTCTTTC 1128
DB 504 GAGCTCTCTCCCCCCTCCCTCCGCGCGCGCGGATACACCCCGCCCTCTCTCTTTC 563
QY 1129 TTTCCTCGTTTTTTTTTTCGCTCGCTCTCGATCTTTGGCTTGGTAGTTGGGATGGGCG 1188
DB 564 TTTCCTCGTTTTTTTTTTCGCTCGCTCTCGATCTTTGGCTTGGTAGTTGGGATGGGCG 623
QY 1189 AGAGCGGCTTCGTGCGCCAGATCGGTGCGCGCGGAGCGCGGAGATCTTCGCGCTGCGCTCT 1248
DB 624 AGAGCGGCTTCGTGCGCCAGATCGGTGCGCGCGGAGCGCGGAGATCTTCGCGCTGCGCTCT 683
QY 1249 CCGGCGCTGAGTCCGCGCCCGGATCTTCGCGGCGGAGATGGGGCTCTCGGATGTAGATCT 1304
DB 684 CCGGCGCTGAGTCCGCGCCCGGATCTTCGCGGCGGAGATGGGGCTCTCGGATGTAGATCT 739

RESULT 14
US-09-991-209-36

```

```
; Sequence 36, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 5164
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pPO10.1 vector
US-09-991-209-36
```

```
Query Match      15.1%; Score 236; DB 10; Length 5164;
Best Local Similarity 100.0%; Pred. No. 1.5e-108;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1069 GAGCTCTCTCCCTCCCTCCCTCCGCGCGCGGTAAACACCCCGCCCTCTCTCTTTTC 1128
          |||
DB      4814 GAGCTCTCTCCCTCCCTCCCTCCGCGCGCGGTAAACACCCCGCCCTCTCTTTTC 4873

QY      1129 TTCTCCGTTTTTTTTTTCGTCGATCTTGACCTTGATTTGGGTGGCG 1188
          |||
DB      4874 TTCTCCGTTTTTTTTTTCGTCGATCTTGACCTTGATTTGGGTGGCG 4933

QY      1189 AGAGCGGCTTCGTCGCCCAATCGGTGCGGAGGCGGATCTCGCGCTGGCTCT 1248
          |||
DB      4934 AGAGCGGCTTCGTCGCCCAATCGGTGCGGAGGCGGATCTCGCGCTGGCTCT 4993

QY      1249 CCGGCGGTGATGCGCGCGGATCTCGCGGGAATGGGGCTTCGATGTAGATCT 1304
          |||
DB      4994 CCGGCGGTGATGCGCGCGGATCTCGCGGGAATGGGGCTTCGATGTAGATCT 5049
```

## RESULT 15

```
US-09-991-209-25
; Sequence 25, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 5277
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pTP5-1 vector
US-09-991-209-25
```

```
Query Match      15.1%; Score 236; DB 10; Length 5277;
Best Local Similarity 100.0%; Pred. No. 1.5e-108;
```

```
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1069 GAGCTCTCTCCCTCCCTCCCTCCGCGCGCGGTAAACACCCCGCCCTCTCTTTTC 1128
          |||
DB      4930 GAGCTCTCTCCCTCCCTCCCTCCGCGCGCGGTAAACACCCCGCCCTCTCTTTTC 4989

QY      1129 TTCTCCGTTTTTTTTTTCGTCGATCTTGACCTTGATTTGGGTGGCG 1188
          |||
DB      4990 TTCTCCGTTTTTTTTTTCGTCGATCTTGACCTTGATTTGGGTGGCG 5049

QY      1189 AGAGCGGCTTCGTCGCCCAATCGGTGCGGAGGCGGATCTCGCGCTGGCTCT 1248
          |||
DB      5050 AGAGCGGCTTCGTCGCCCAATCGGTGCGGAGGCGGATCTCGCGCTGGCTCT 5109

QY      1249 CCGGCGGTGATGCGCGCGGATCTCGCGGGAATGGGGCTTCGATGTAGATCT 1304
          |||
DB      5110 CCGGCGGTGATGCGCGCGGATCTCGCGGGAATGGGGCTTCGATGTAGATCT 5165
```

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Job time : 831.171 secs
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